



Las epidemias que vendrán en el siglo XXI

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Vigo, 7 de octubre de 2022

THE
BEATLES

Tomorrow never knows

THE
BEATLES



«Tomorrow Never Knows»

Canción de The Beatles

Álbum	<i>Revolver</i>
Publicación	5 de agosto de 1966
Grabación	EMI Studios, Londres (6, 7 y 22 de abril de 1966)
Género	Rock psicodélico, ^{1 2} rock experimental, ³ Art rock Raga rock Drone rock Avant-pop
Duración	2:57
Discográfica	Parlophone
Escritor(es)	Lennon-McCartney
Productor(es)	George Martin
Idioma original	inglés

<https://www.youtube.com/watch?v=pHNbHn3i9S4>

Mañana nunca se sabe

¿Método científico?

- **Científico**

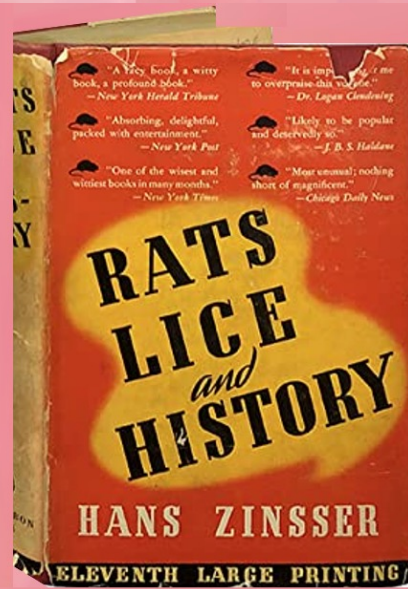
Persona que se dedica a la investigación y estudio de una ciencia.

- **Método Científico**

Que se ajusta a los principios y métodos de la ciencia.







"A very book, a witty book, a profound book."
— *New York Herald Tribune*

"Absorbing, delightful, packed with entertainment."
— *New York Post*

"One of the wisest and wisest books in many months."
— *New York Times*

"It is impossible for me to overpraise this volume."
— *Dr. Eugen Ganderberg*

"Likely to be popular and deservedly so."
— *J. B. S. Haldane*

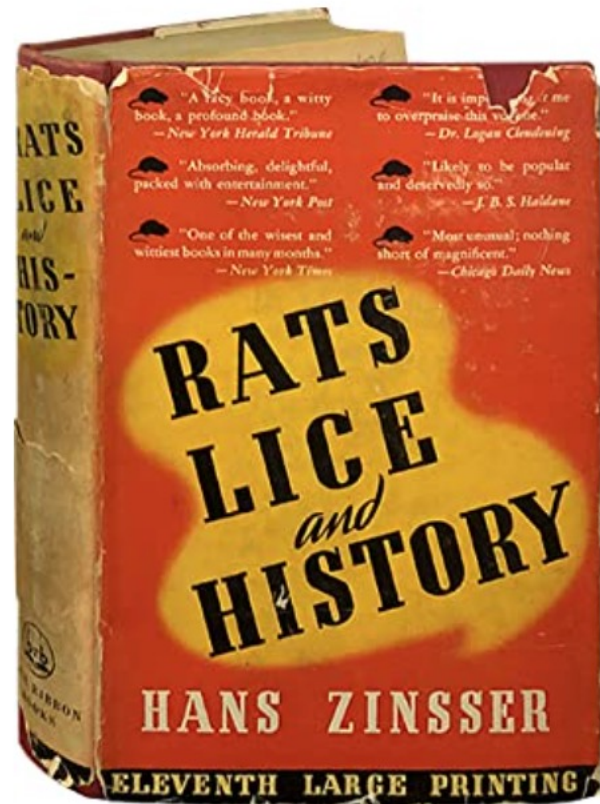
"Most unusual; nothing short of magnificent."
— *Chicago Daily News*

RATS LICE and HISTORY

HANS ZINSSER

ELEVENTH LARGE PRINTING

“Las enfermedades infecciosas están cambiando constantemente, las nuevas se encuentran en proceso de desarrollo mientras que las antiguas están siendo modificadas o desapareciendo”

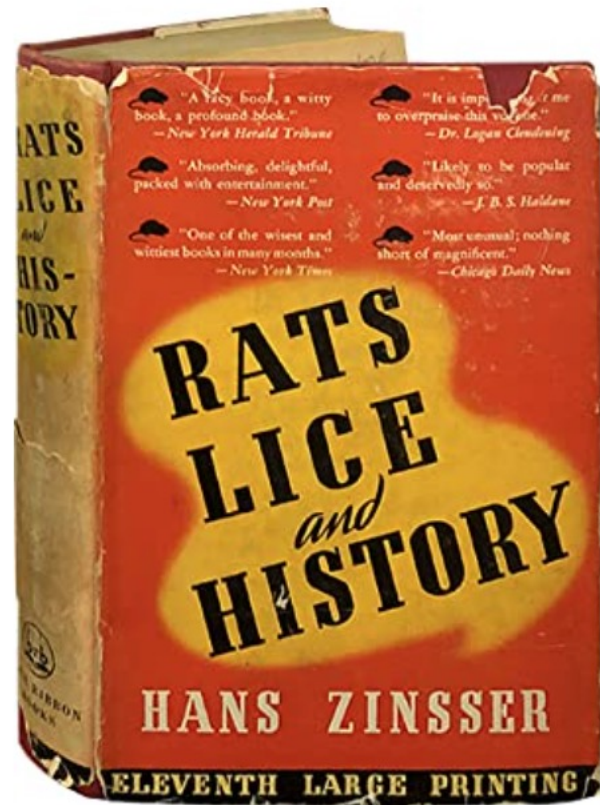


(1935)



(1878-1940)

“Nada en el mundo de las criaturas vivas permanece estable ”



(1935)



(1878-1940)

CALENDARIOS ANUALES

Zika, Crimea-Congo, Dengue,
Oeste del Nilo, **COVID-19**
Monkeypox



Monkeypox



Sábado 23 de julio de 2022

Declaración de la viruela del mono como emergencia de Salud Pública de Importancia Internacional

CALENDARIOS ANUALES

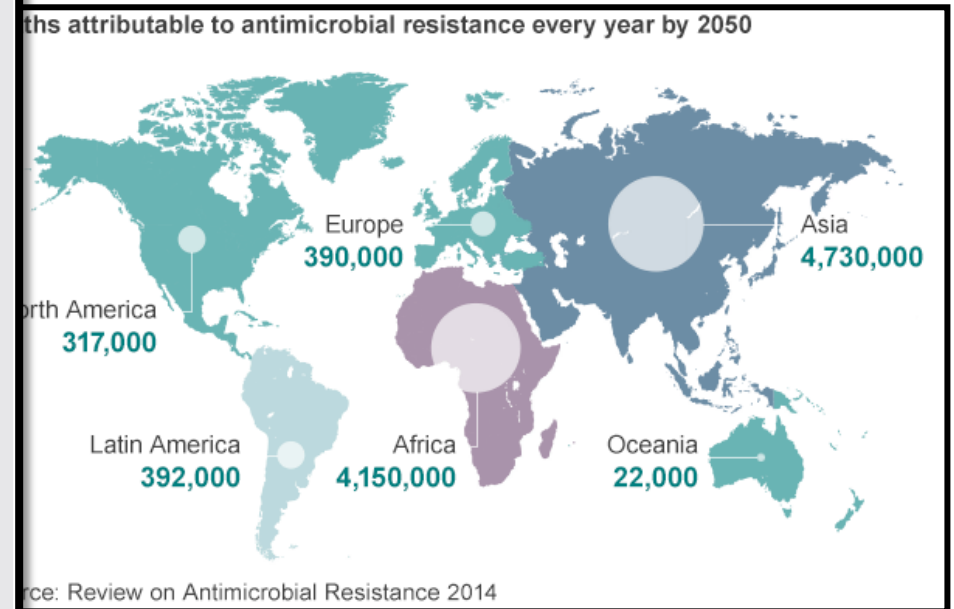
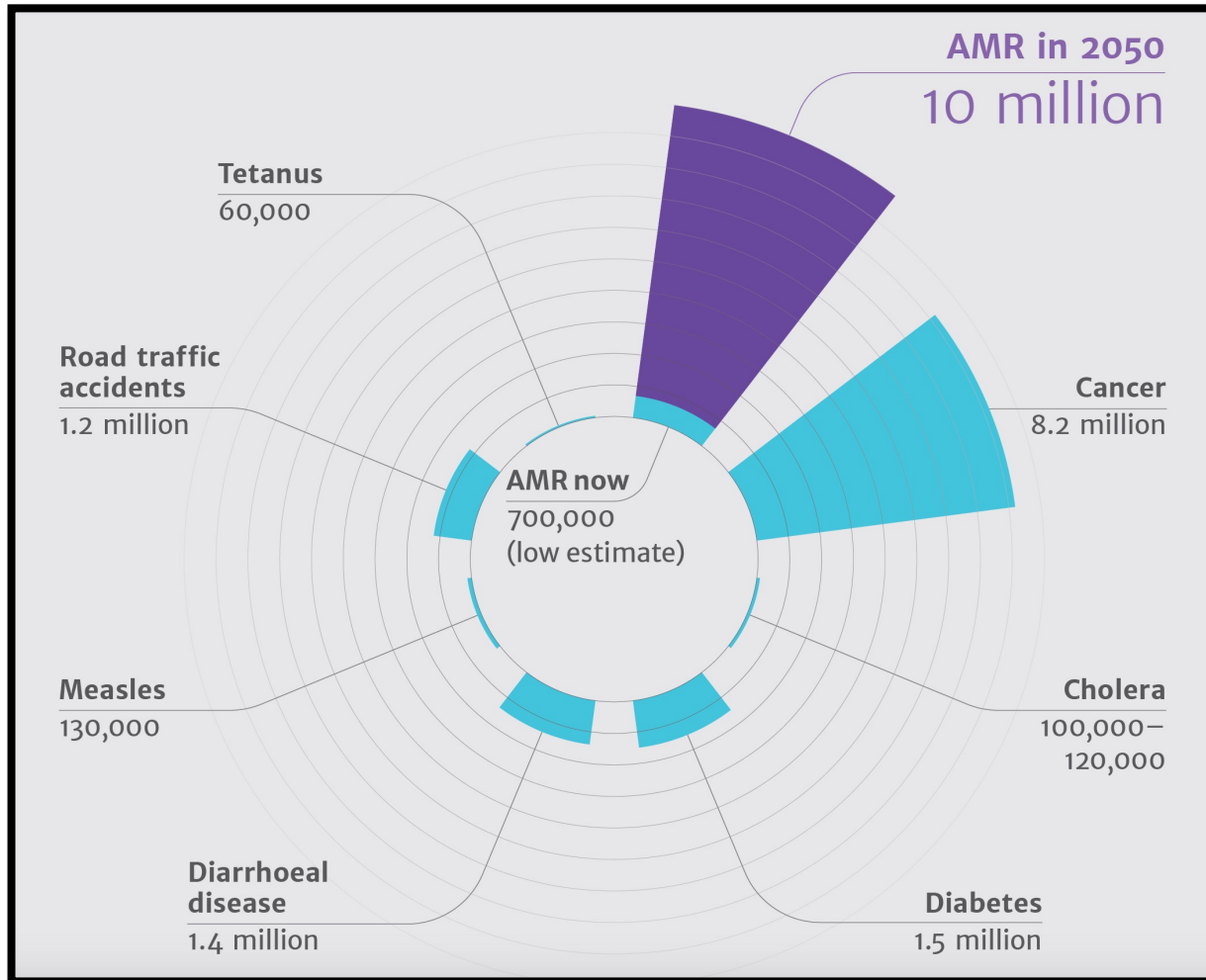
¿cuál será la próxima?



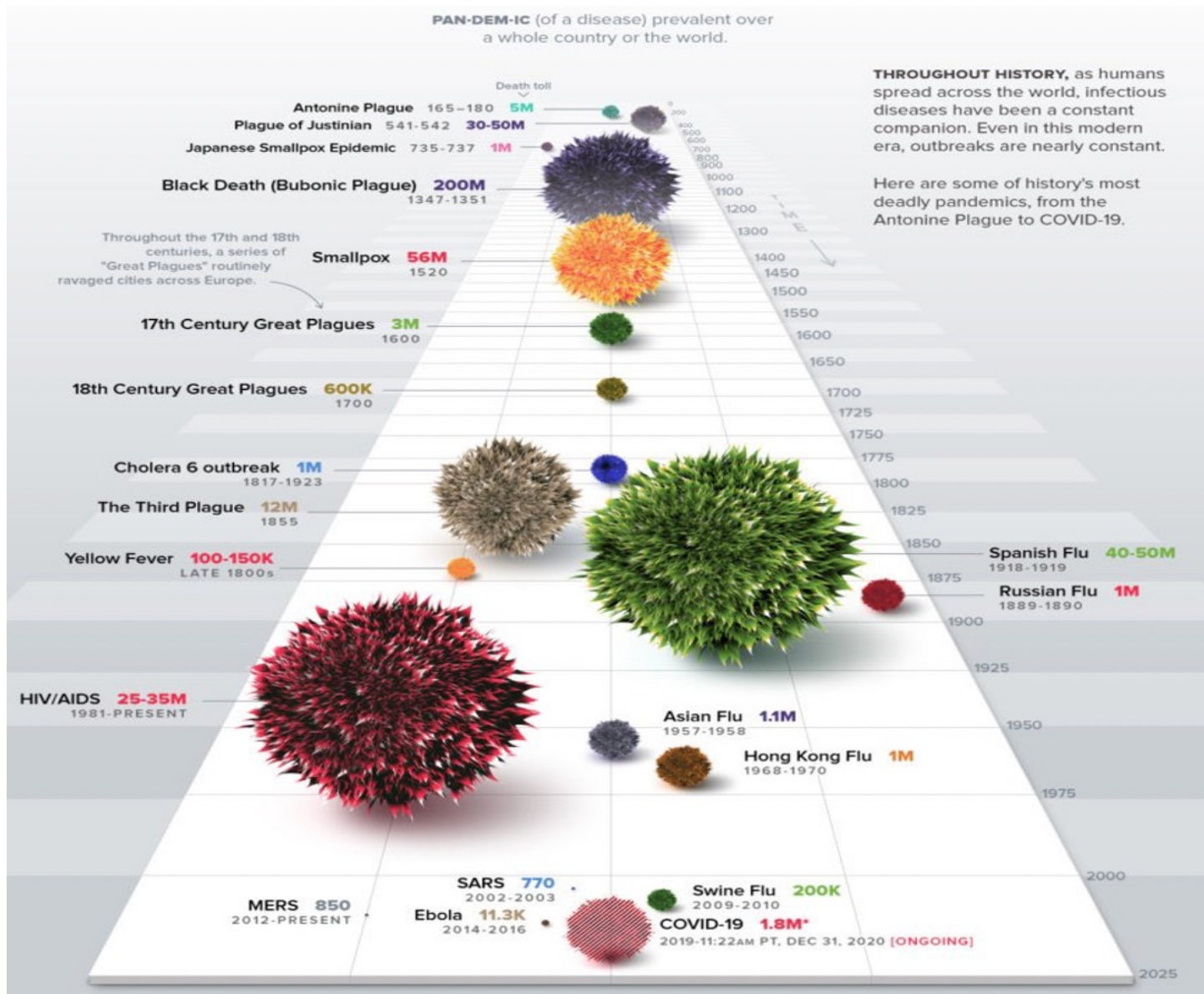
Departamento de
Enfermedades Infecciosas



Principales causas de muerte en 2050

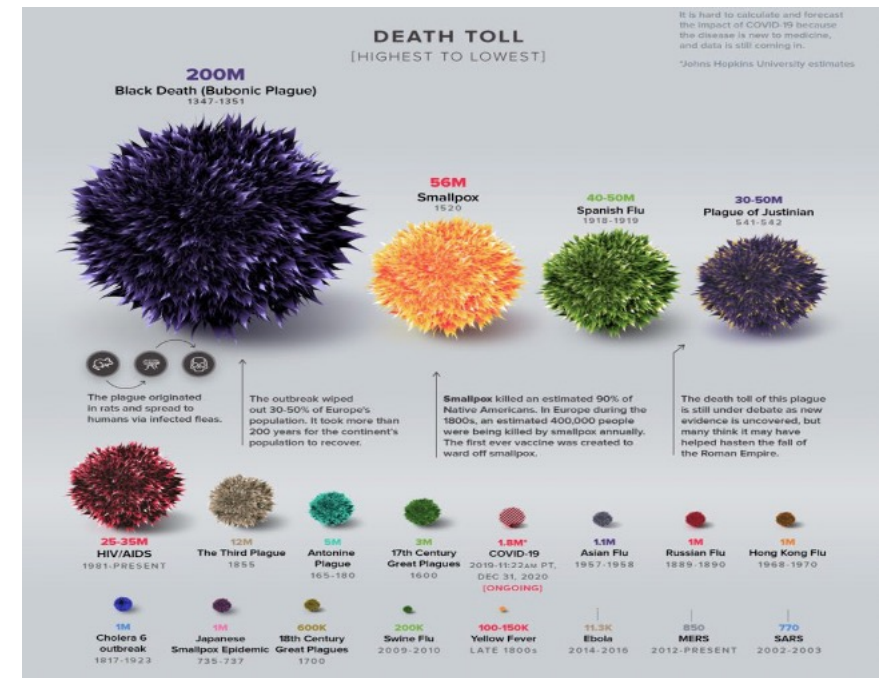


La resistencia bacteriana a antibióticos será la principal causa de muerte en 2050



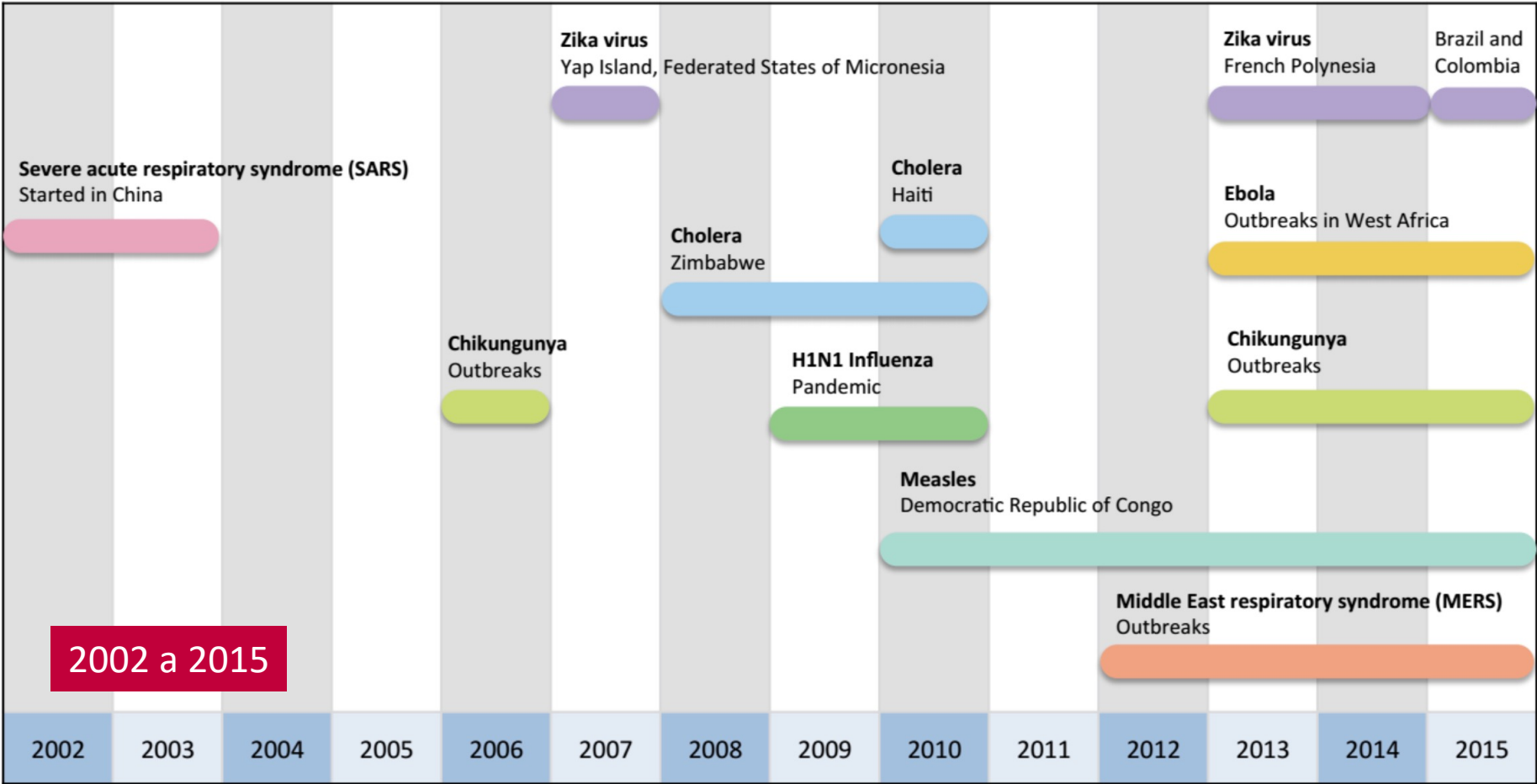
Historia de las PANDEMIAS

<https://pbs.twimg.com/media/EsvBnJdXAAEwp0v?format=jpg&name=large>

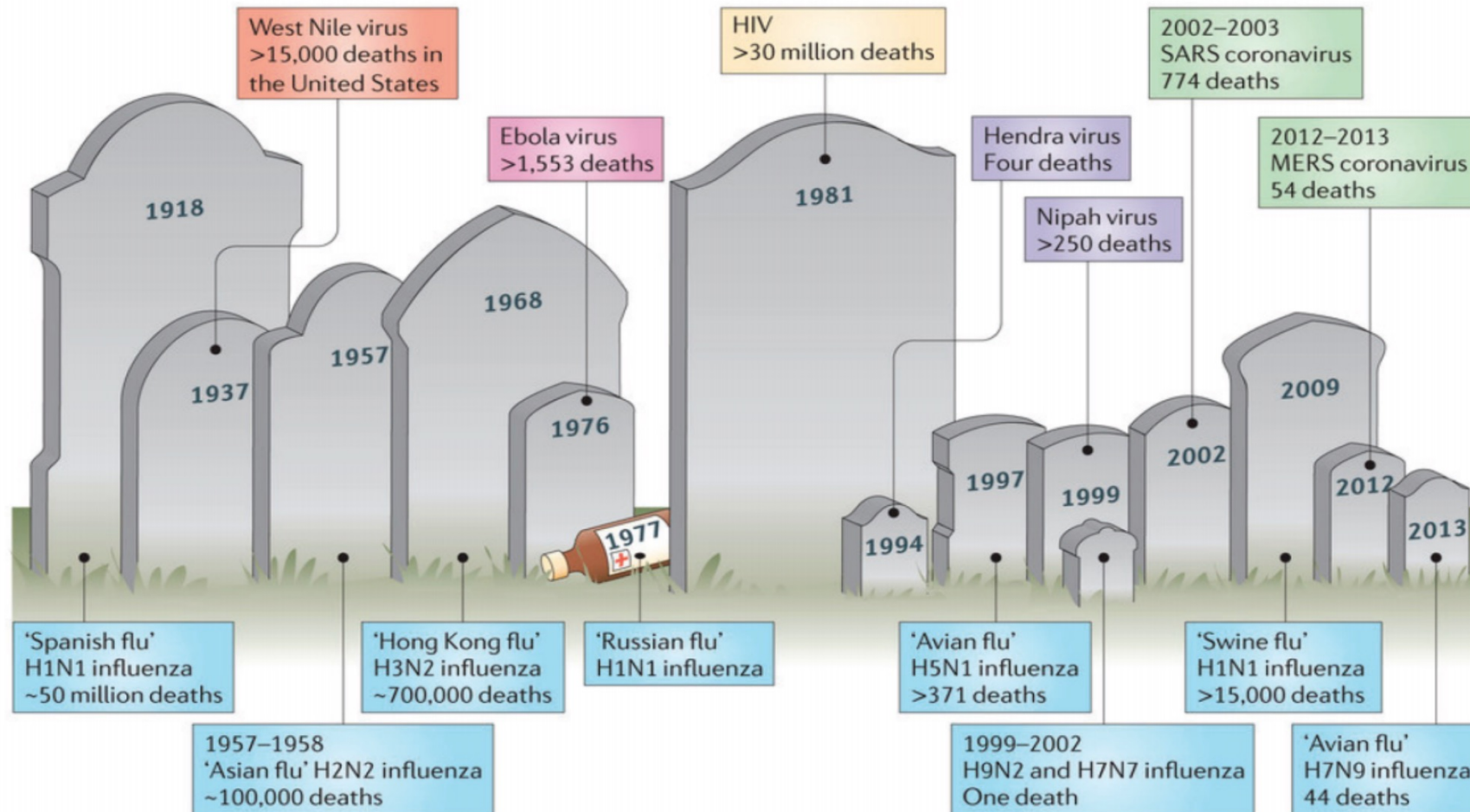


En la historia de las grandes epidemias las infecciones bacterianas han tenido gran peso

Enfermedades Infecciosas Emergentes y Reemergentes mayores



Defunciones asociadas a epidemias de virus emergentes y re-emergentes



Evolución de la Pandemia por SARS-CoV-2 y COVID-19

Tracking Home Data Visualizations **Global Map** U.S. Map Data in Motion Tracking FAQ

 COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU)

Last Updated at (M/D/YYYY)
26/9/2022, 17:23

Total Cases
615.203.142

Total Deaths
6.537.363

Total Vaccine Doses Administered
12.253.797.161

Cases | Deaths by
Country/Region/Sovereignty

28-Day Cases
14.106.499

28-Day Deaths
49.084

28-Day Vaccine Doses Administered
118.735.214

Japan
28-Day: **2.528.281** | 5.354
Totals: **21.060.235** | 44.401

US
28-Day: **1.851.251** | 12.234
Totals: **96.079.338** | 1.056.477

Korea, South
28-Day: **1.607.336** | 1.628
Totals: **24.634.296** | 28.246

Russia
28-Day: **1.370.229** | 2.634
Totals: **20.533.598** | 379.019

Taiwan*
28-Day: **1.028.466** | 984
Totals: **6.278.794** | 10.884

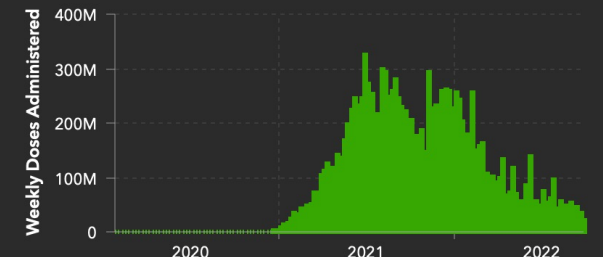
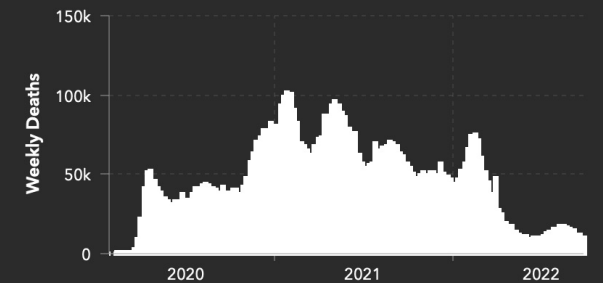
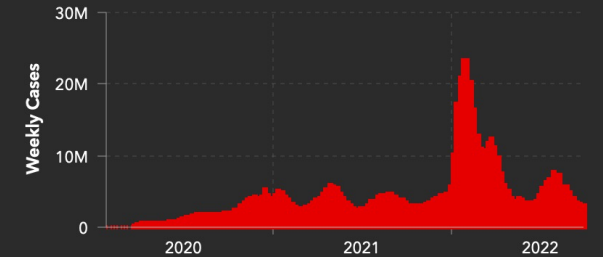
Germany
28-Day: **910.700** | 2.354
Totals: **32.952.050** | 149.458

France
28-Day: **641.814** | 1.030
Totals: **35.304.648** | 155.927



Esri, FAO, NOAA, USGS

Powered by Esri



Admin0

28-Day

Totals

Incidence

Case-Fatality Ratio

Global Vaccinations

US Vaccinations

Terms of Use

Weekly

28-Day



14.9 million excess deaths associated with the COVID-19 pandemic in 2020 and 2021

5 May 2022 | News release | Reading time: 3 min (852 words)

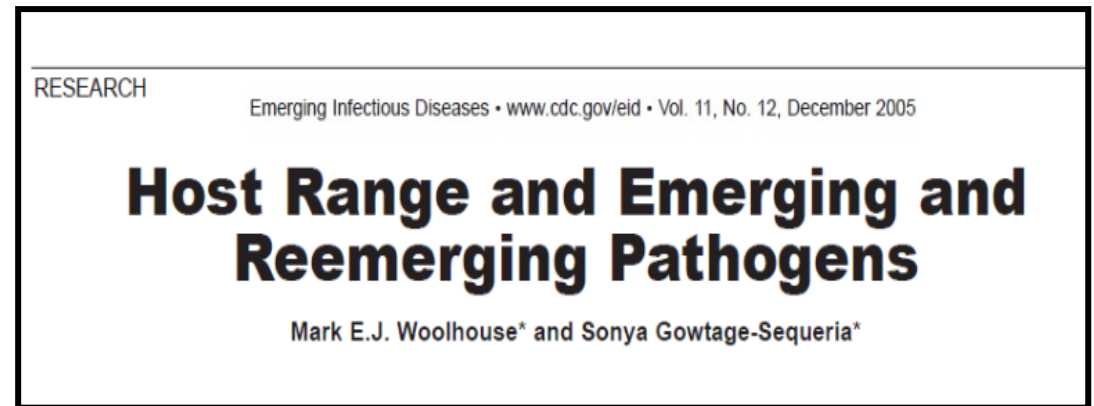
¿De dónde nos
vienen las amenazas?

¿De donde nos vienen las amenazas?

De las más de 1.400 agentes patógenos humanos



Al menos el 60% son de origen zoonótico

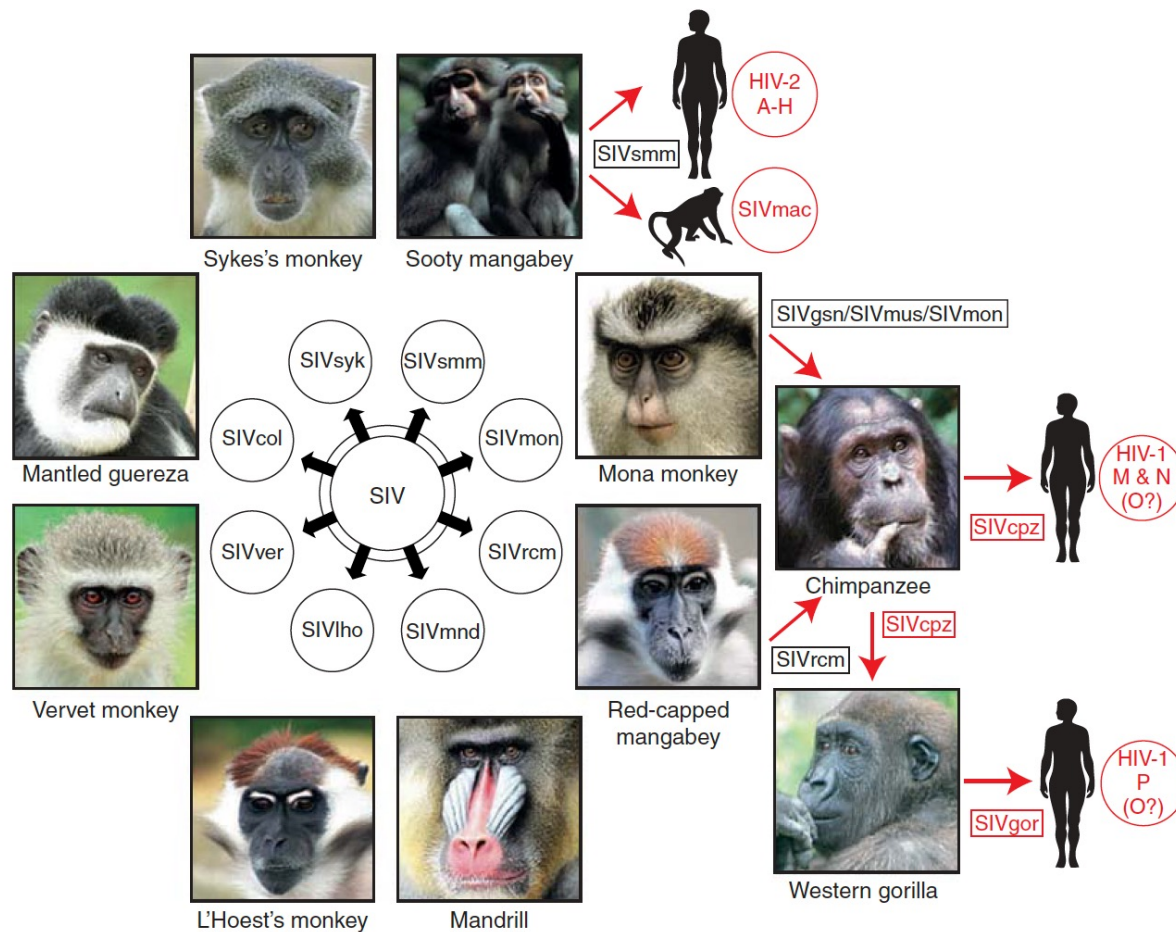


> 60% de las infecciones que sufrimos son de origen zoonótico



85 % de las amenazas actuales son de origen zoonótico

¿Cuál es origen del VIH?



Sharp PM & Hahn BH. 2011

Adaptación y cruce del SIV en diferentes especies de simio

Origen del VIH

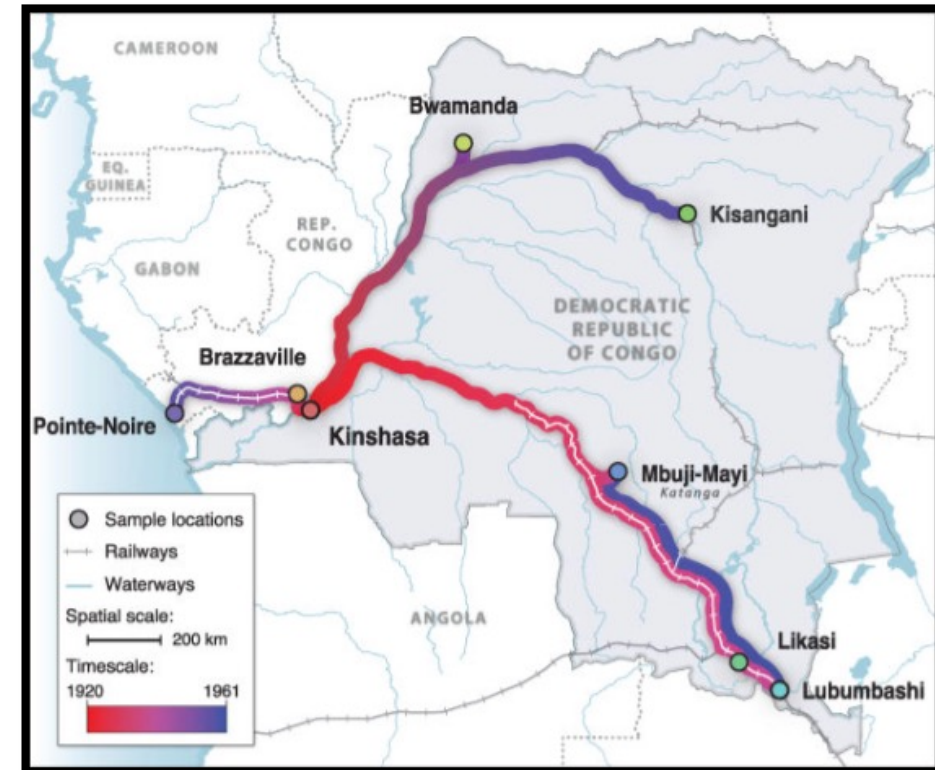
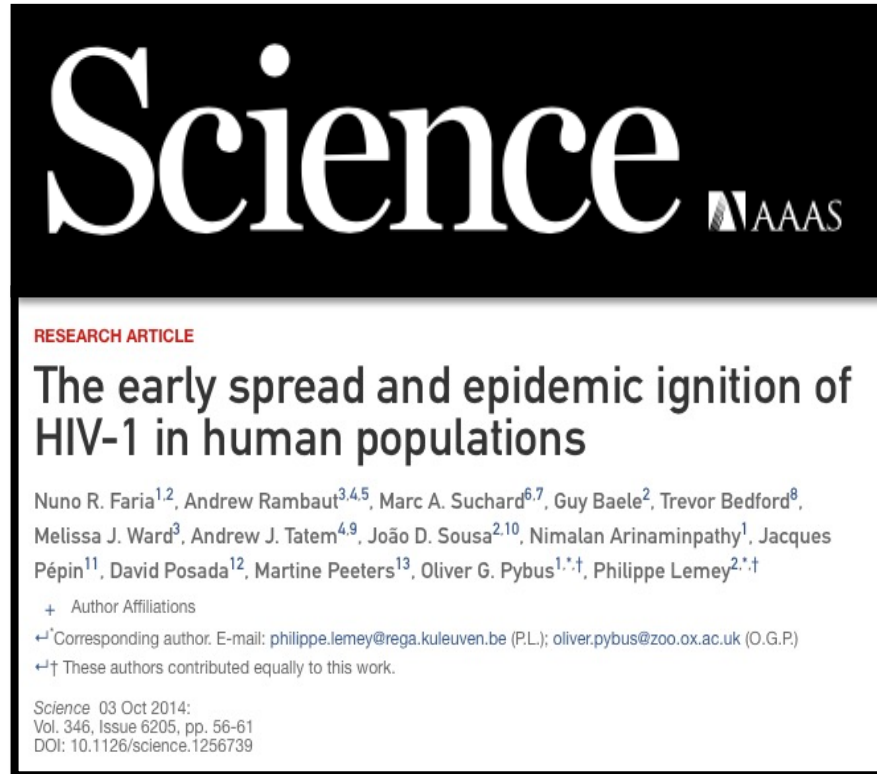


Pan troglodytes troglodytes

Gorilla gorilla

Salto y adaptación del (SIV y SIVgor) al humano por rituales asociadas a la caza

Origen de la epidemia



Transmisión humana eficiente mediante contacto sexual y otras

Posible origen en Zaire (actual RDC) en los años 20
Expansión por África siguiendo rutas de comunicación



1970s and 'Patient 0' HIV-1 genomes illuminate early HIV/AIDS history in North America

Michael Worobey, Thomas D. Watts, Richard A. McKay, Marc A. Suchard, Timothy Granade, Dirk E. Teuwen, Beryl A. Koblin, Walid Heneine, Philippe Lemey & Harold W. Jaffe

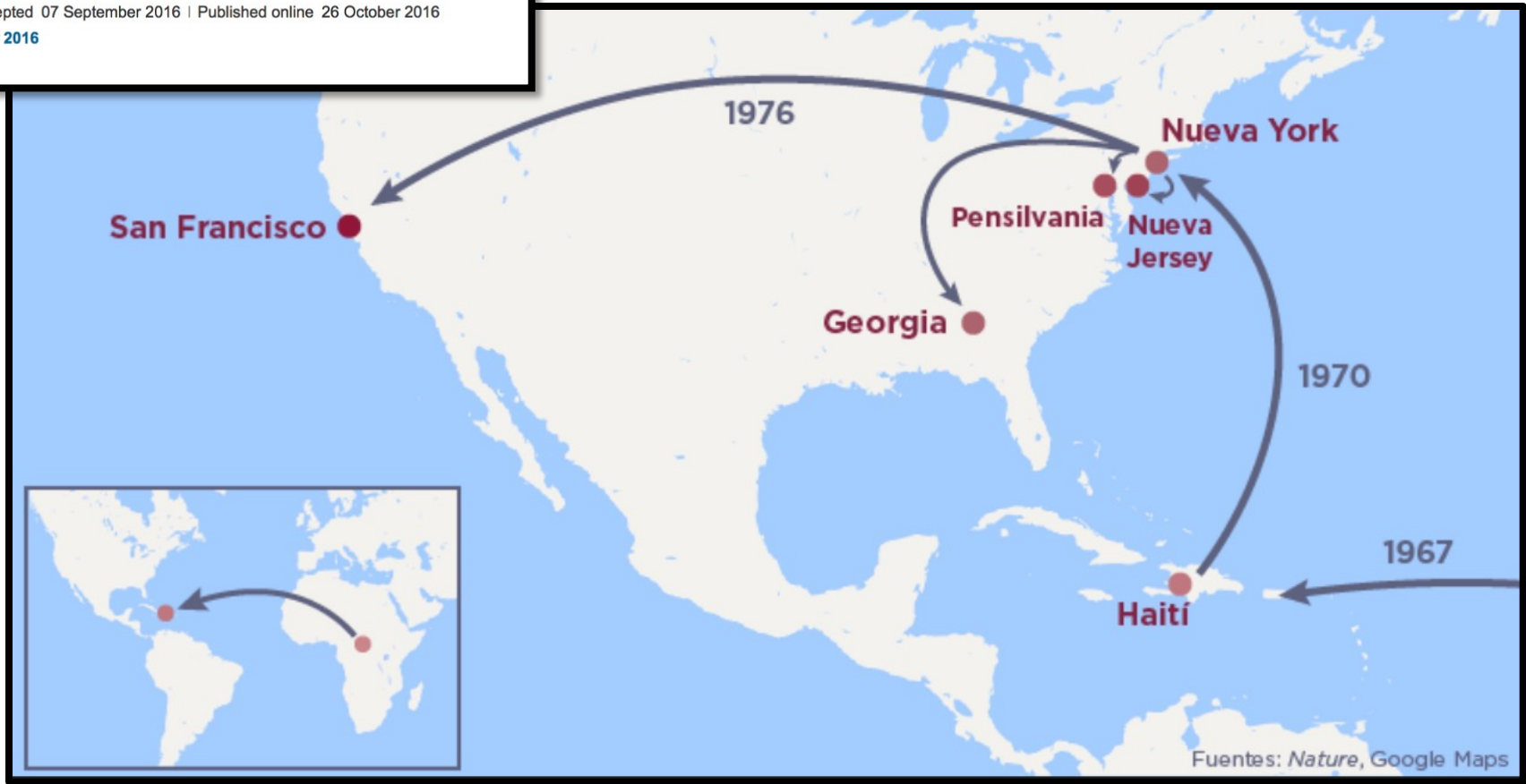
[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

Nature 539, 98–101 (03 November 2016) | doi:10.1038/nature19827

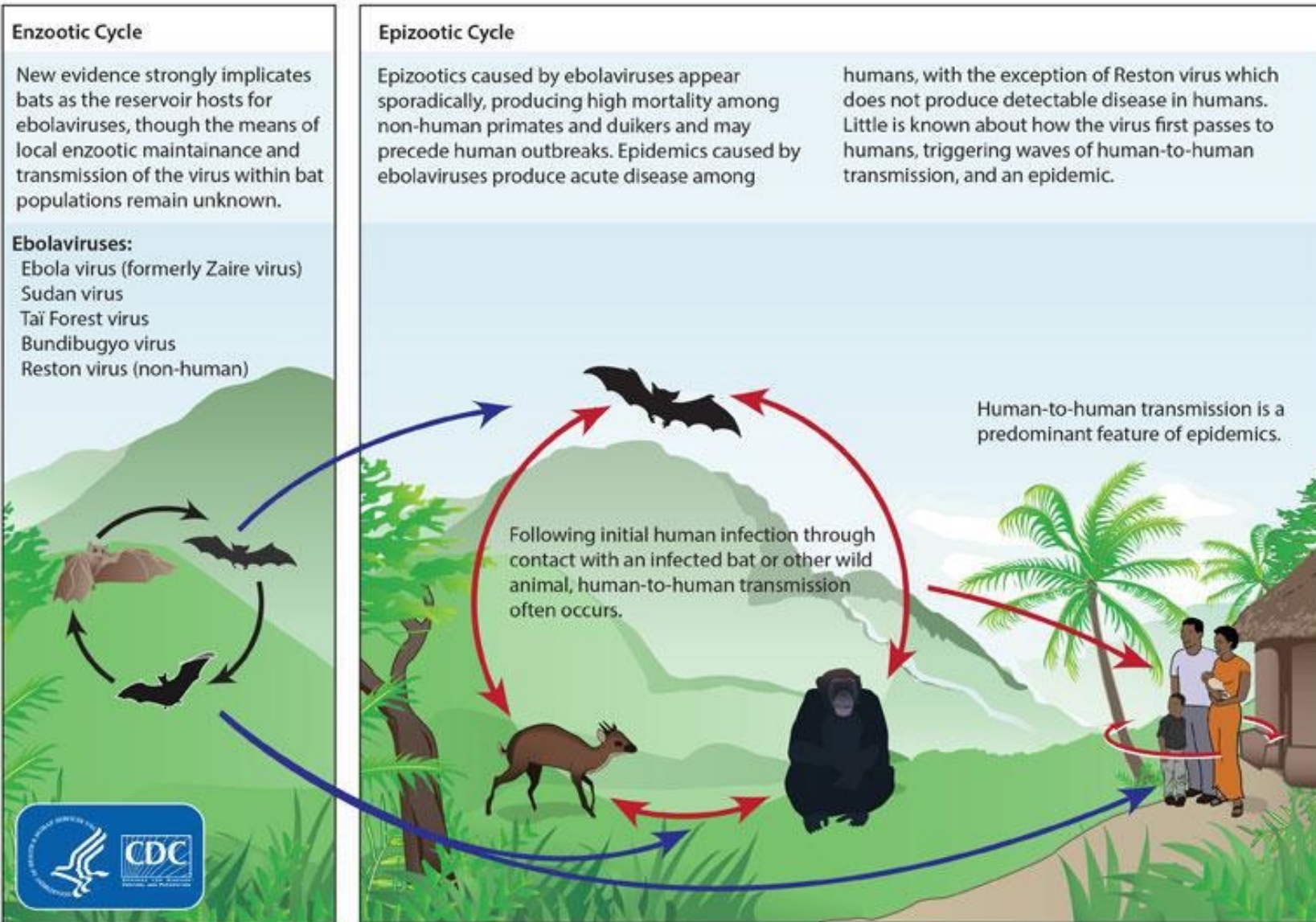
Received 05 April 2016 | Accepted 07 September 2016 | Published online 26 October 2016

| Corrected online 02 October 2016

Expansión del VIH



Ecología de los virus Ebola



¿Cómo ha surgido el SARS-CoV-2?

Science

INSIGHTS | PERSPECTIVES

VIEWPOINT: COVID-19

The animal origin of SARS-CoV-2

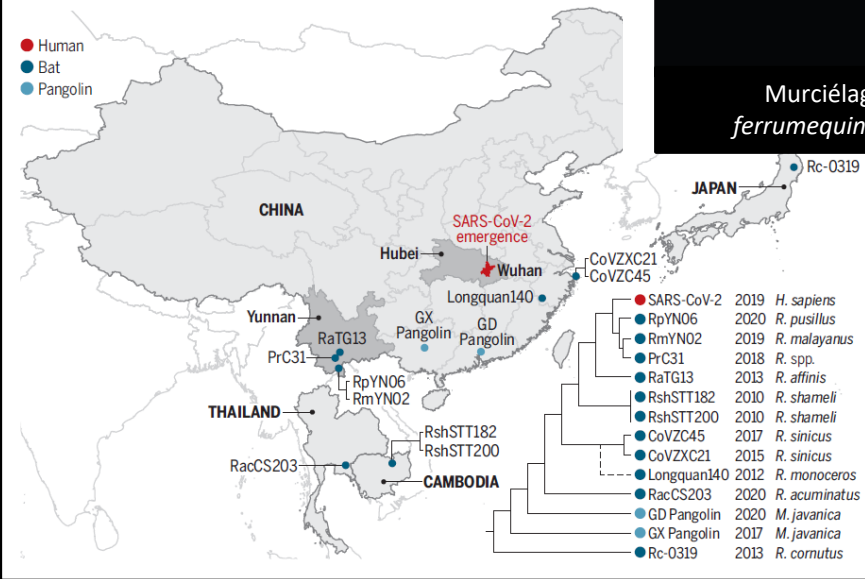
Trading of animals susceptible to bat coronaviruses is the likely cause of the COVID-19 pandemic

By Spyros Lytras¹, Wei Xia², Joseph Hughes¹, Xiaowei Jiang³, David L. Robertson¹

27 AUGUST 2021 • VOL 373 ISSUE 6558 969

Sarbecoviruses closely related to SARS-CoV-2

Coronaviruses that are evolutionarily closest to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have been sampled in China, Cambodia, Japan, and Thailand (5). The phylogenetic tree, inferred for recombination (5), shows sarbecoviruses closely related to SARS-CoV-2. Host species include *Rhinolophus* (bat), human (*Homo sapiens*), and pangolin (*Manis javanica*) and the year of sampling. Longquan140 is inferred from another genomic region (5) (dashed line). See supplemental



Origen animal del SARS-CoV-2

Spillover

SARS-CoVs

Interacción con animales que expresan el receptor de entrada del virus



Interacción con los humanos



¿Cómo ha surgido la epidemia de COVID-19

RESEARCH

Science **377**, 951–959 (2022) 26 August 2022

CORONAVIRUS

The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic

Michael Worobey^{1*}, Joshua I. Levy², Lorena Malpica Serrano¹, Alexander Crits-Christoph³, Jonathan E. Pekar^{4,5}, Stephen A. Goldstein⁶, Angela L. Rasmussen^{7,8}, Moritz U. G. Kraemer⁹, Chris Newman¹⁰, Marion P. G. Koopmans^{11,12}, Marc A. Suchard^{13,14,15}, Joel O. Wertheim¹⁶, Philippe Lemey^{17,18}, David L. Robertson¹⁹, Robert F. Garry^{18,20,21}, Edward C. Holmes²², Andrew Rambaut²³, Kristian G. Andersen^{2,24*}

Understanding how severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in 2019 is critical to preventing future zoonotic outbreaks before they become the next pandemic. The Huanan Seafood Wholesale Market in Wuhan, China, was identified as a likely source of cases in early reports, but later this conclusion became controversial. We show here that the earliest known COVID-19 cases from December 2019, including those without reported direct links, were geographically centered on this market. We report that live SARS-CoV-2-susceptible mammals were sold at the market in late 2019 and that within the market, SARS-CoV-2-positive environmental samples were spatially associated with vendors selling live mammals. Although there is insufficient evidence to define upstream events, and exact circumstances remain obscure, our analyses indicate that the emergence of SARS-CoV-2 occurred through the live wildlife trade in China and show that the Huanan market was the epicenter of the COVID-19 pandemic.

<https://www.science.org/doi/epdf/10.1126/science.abp8715>

RESEARCH

Science **377**, 960–966 (2022) 26 August 2022

CORONAVIRUS

The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2

Jonathan E. Pekar^{1,2*}, Andrew Magee³, Edyth Parker⁴, Niema Moshiri⁵, Katherine Izhikevich^{5,6}, Jennifer L. Havens¹, Karthik Gangavarapu³, Lorena Mariana Malpica Serrano⁷, Alexander Crits-Christoph⁸, Nathaniel L. Matteson⁴, Mark Zeller⁴, Joshua I. Levy⁴, Jade C. Wang⁹, Scott Hughes⁹, Jungmin Lee¹⁰, Heedo Park^{10,11}, Man-Seong Park^{10,11}, Katherine Ching Zi Yan¹², Raymond Tzer Pin Lin¹², Mohd Noor Mat Isa¹³, Yusuf Muhammad Noor¹³, Tetyana I. Vasylyeva¹⁴, Robert F. Garry^{15,16,17}, Edward C. Holmes¹⁸, Andrew Rambaut¹⁹, Marc A. Suchard^{3,20,21*}, Kristian G. Andersen^{4,22*}, Michael Worobey^{7*}, Joel O. Wertheim^{14*}

Understanding the circumstances that lead to pandemics is important for their prevention. We analyzed the genomic diversity of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) early in the coronavirus disease 2019 (COVID-19) pandemic. We show that SARS-CoV-2 genomic diversity before February 2020 likely comprised only two distinct viral lineages, denoted “A” and “B.” Phylodynamic rooting methods, coupled with epidemic simulations, reveal that these lineages were the result of at least two separate cross-species transmission events into humans. The first zoonotic transmission likely involved lineage B viruses around 18 November 2019 (23 October to 8 December), and the separate introduction of lineage A likely occurred within weeks of this event. These findings indicate that it is unlikely that SARS-CoV-2 circulated widely in humans before November 2019 and define the narrow window between when SARS-CoV-2 first jumped into humans and when the first cases of COVID-19 were reported. As with other coronaviruses, SARS-CoV-2 emergence likely resulted from multiple zoonotic events.

<https://www.science.org/doi/epdf/10.1126/science.abp8337>

Origen en un mercado de venta de animales silvestres vivos en Wuhan (Hubei) /China en diciembre 2019

¿Cómo ha surgido la epidemia de COVID-19

RESEARCH

Science 377, 951–959 (2022) 26 August 2022

CORONAVIRUS

The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic

Michael Worobey^{1*}, Joshua I. Levy², Lorena Malpica Serrano¹, Alexander Crits-Christoph³, Jonathan E. Pekar^{4,5}, Stephen A. Goldstein⁶, Angela L. Rasmussen^{7,8}, Moritz U. G. Kraemer⁹, Chris Newman¹⁰, Marion P. G. Koopmans^{11,12}, Marc A. Suchard^{13,14,15}, Joel O. Wertheim¹⁶, Philippe Lemey^{17,18}, David L. Robertson¹⁹, Robert F. Garry^{18,20,21}, Edward C. Holmes²², Andrew Rambaut²³, Kristian G. Andersen^{2,24*}

Understanding how severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in 2019 is critical to preventing future zoonotic outbreaks before they become the next pandemic. The Huanan Seafood Wholesale Market in Wuhan, China, was identified as a likely source of cases in early reports, but later this conclusion became controversial. We show here that the earliest known COVID-19 cases from December 2019, including those without reported direct links, were geographically centered on this market. We report that live SARS-CoV-2-susceptible mammals were sold at the market in late 2019 and that within the market, SARS-CoV-2-positive environmental samples were spatially associated with vendors selling live mammals. Although there is insufficient evidence to define upstream events, and exact circumstances remain obscure, our analyses indicate that the emergence of SARS-CoV-2 occurred through the live wildlife trade in China and show that the Huanan market was the epicenter of the COVID-19 pandemic.

Table 1. Live mammals traded at the Huanan market in November and December 2019.

Species (susceptibility*)	Family (susceptibility*)	Order (susceptibility*)	Observed at Huanan market November 2019
Raccoon dog (<i>Nyctereutes procyonoides</i>) (Y)	Canidae (Y)	Carnivora (Y)	Y
Amur hedgehog (<i>Erinaceus amurensis</i>)	Erinaceidae	Eulipotyphla	Y
Hog badger (<i>Arctonyx albogularis</i>) (Y)	Mustelidae (Y)	Carnivora (Y)	Y
Asian badger (<i>Meles leucurus</i>)	Mustelidae (Y)	Carnivora (Y)	Y
Chinese hare (<i>Lepus sinensis</i>)	Leporidae (Y)	Lagomorpha (Y)	Y
Chinese bamboo rat (<i>Rhizomys sinensis</i>) (Y)	Spalacidae (Y)	Rodentia (Y)	Y
Malayan porcupine (<i>Hystrix brachyura</i>)	Hystriidae	Rodentia (Y)	Y
Chinese muntjac (<i>Muntiacus reevesi</i>)	Cervidae (Y)	Artiodactyla (Y)	Y
Marmot (<i>Marmota himalayana</i>)	Sciuridae	Rodentia (Y)	Y
Red fox (<i>Vulpes vulpes</i>) (Y)	Canidae (Y)	Carnivora (Y)	Y
Siberian weasel (<i>Mustela sibirica</i>)	Mustelidae (Y)	Carnivora (Y)	N†
Pallas's squirrel (<i>Callosciurus erythraeus</i>)	Sciuridae	Rodentia (Y)	N
Masked palm civet (<i>Paguma larvata</i>) (Y)	Viverridae (Y)	Carnivora (Y)	N
Coypu (<i>Myocastor coypus</i>)	Echimyidae	Rodentia (Y)	N
Mink (<i>Neovison vison</i>) (Y)	Mustelidae (Y)	Carnivora (Y)	N
Red squirrel (<i>Sciurus vulgaris</i>)	Sciuridae	Rodentia (Y)	N
Wild boar (<i>Sus scrofa</i>) (Y)	Suidae (Y)	Artiodactyla (Y)	N
Complex-toothed flying squirrel (<i>Trogopterus xanthipes</i>)	Sciuridae	Rodentia (Y)	N

*Based on live susceptibility findings, serological findings, or ACE2-binding assays. See table S5 for details and associated references.

†Animals listed as "N" (no) were, however, present at Wuhan market during the 2017–2019 study period (8).

<https://www.science.org/doi/epdf/10.1126/science.abp8715>

Venta de animales vivos susceptibles al SARS-CoV-2 en las fechas de comienzo de la epidemia

Cite as: M. Worobey *et al.*, *Science*
10.1126/science.abp8715 (2022).

The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic

Michael Worobey^{1*}, Joshua I. Levy², Lorena Malpica Serrano¹, Alexander Crits-Christoph³, Jonathan E. Pekar^{4,5}, Stephen A. Goldstein⁶, Angela L. Rasmussen^{7,8}, Moritz U. G. Kraemer⁹, Chris Newman¹⁰, Marion P. G. Koopmans^{11,12}, Marc A. Suchard^{13,14,15}, Joel O. Wertheim¹⁶, Philippe Lemey^{17,18}, David L. Robertson¹⁹, Robert F. Garry^{18,20,21}, Edward C. Holmes²², Andrew Rambaut²³, Kristian G. Andersen^{2,24*}



<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9348750/pdf/science.abp8715.pdf>

La emergencia de la COVID-19 se produjo por el comercio de animales infectados

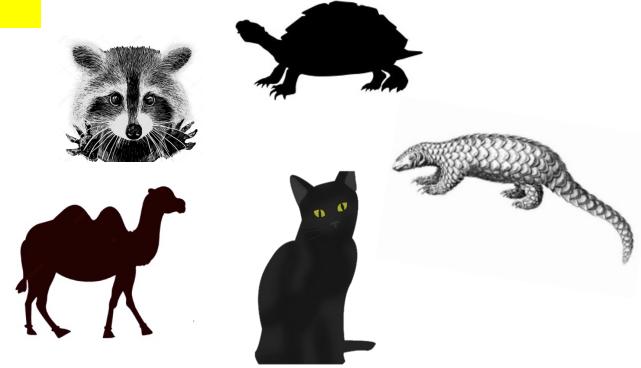


Mapache

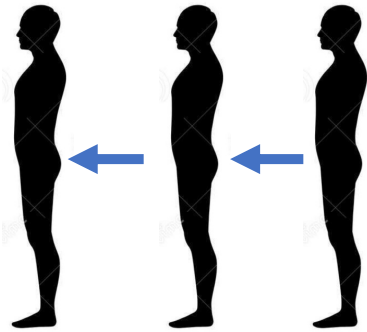
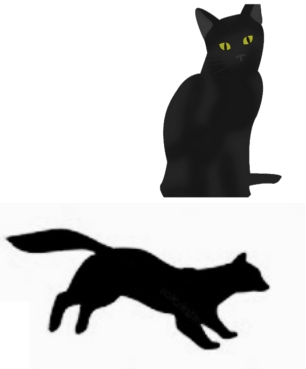
Spillover

SARS-CoV-2

Interacción con animales que expresan el receptor de entrada del virus



Interacción con los humanos



Transmisión entre humanos por vía aérea

> *Transbound Emerg Dis.* 2020 Aug 18;10.1111/tbed.13803. doi: 10.1111/tbed.13803.
Online ahead of print.

Detection of SARS-CoV-2 in pets living with COVID-19 owners diagnosed during the COVID-19 lockdown in Spain: A case of an asymptomatic cat with SARS-CoV-2 in Europe

Ignacio Ruiz-Arrondo ¹, Aránzazu Portillo ¹, Ana M Palomar ¹, Sonia Santibáñez ¹, Paula Santibáñez ¹, Cristina Cervera ¹, José A Oteo ¹



Science

REPORTS

Cite as: B. B. Oude Munnink *et al.*, *Science* 10.1126/science.abe5901 (2020).

Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans

Bas B. Oude Munnink^{1*}, Reina S. Sikkema¹, David F. Nieuwenhuijse¹, Robert Jan Molenaar², Emmanuelle Munger¹, Richard Molenkamp¹, Arco van der Spek¹, Paulien Tolsma¹, Ariene Rietveld³, Miranda Brouwer¹, Noortje Bouwmeester-Vincken⁴, Frank Harders⁵, Renate Hakze-van der Honing⁶, Marjolein C. A. Wegdam-Blans⁷, Ruth J. Bouwstra⁸, Corine GeurtsvanKessel¹, Annemiek A. van der Eijk¹, Francisca C. Velkers⁹, Lidwien A. M. Smit¹⁰, Arjan Stegeman¹¹, Wim H. M. van der Poel¹², Marion P. G. Koopmans¹

¹Erasmus MC, Department of Viroscience, WHO collaborating centre for arbovirus and viral hemorrhagic fever Reference and Research, Rotterdam, Netherlands. ²Royal GD, Deventer, Netherlands. ³Netherlands Food and Consumer Product Safety Authority (NVWA), Utrecht, Netherlands. ⁴Municipal health Services GGD Brabant-Zuidoost, Eindhoven, Netherlands. ⁵Municipal health Services GGD Hart voor Brabant. ⁶Herfogenbosch, Netherlands. ⁷Municipal health Services GGD Limburg-Noord, Venlo, Netherlands. ⁸Wageningen Bioveterinary Research, Lelystad, Netherlands. ⁹Sliciting PAMM, Veldhoven, Netherlands. ¹⁰Farm Animal Health, Utrecht University, Utrecht, Netherlands. ¹¹Institute for Risk Assessment Sciences (IRAS), Utrecht University, Utrecht, Netherlands.

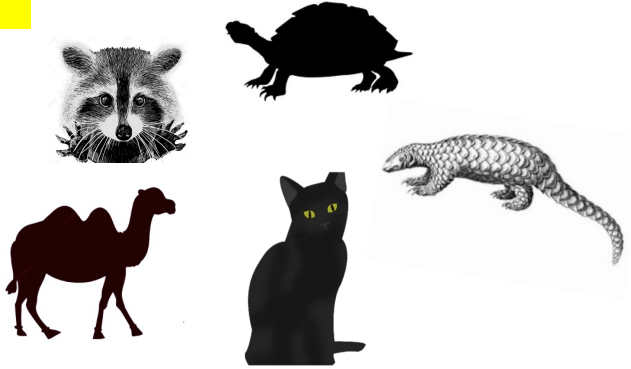
Humanos como fuente de infección
para otros animales



Spillover

SARS-CoV-2

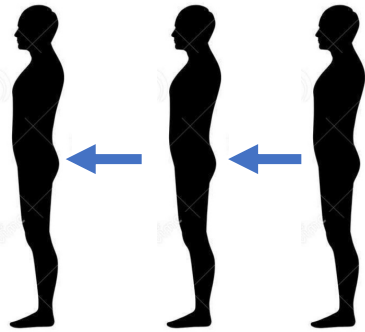
Interacción con animales que expresan el receptor de entrada del virus



Interacción con los humanos



Diseminación mediante viajes



Transmisión entre humanos

En un tiempo menor que el periodo de incubación de la mayoría de las Enfermedades Infecciosas, podemos estar en cualquier parte del planeta





1964
The Beatles arrive at
JFK, New York



1976
First supersonic
Concorde flight
takes off

1990
Europe's first
low-cost airline
tickets go on sale

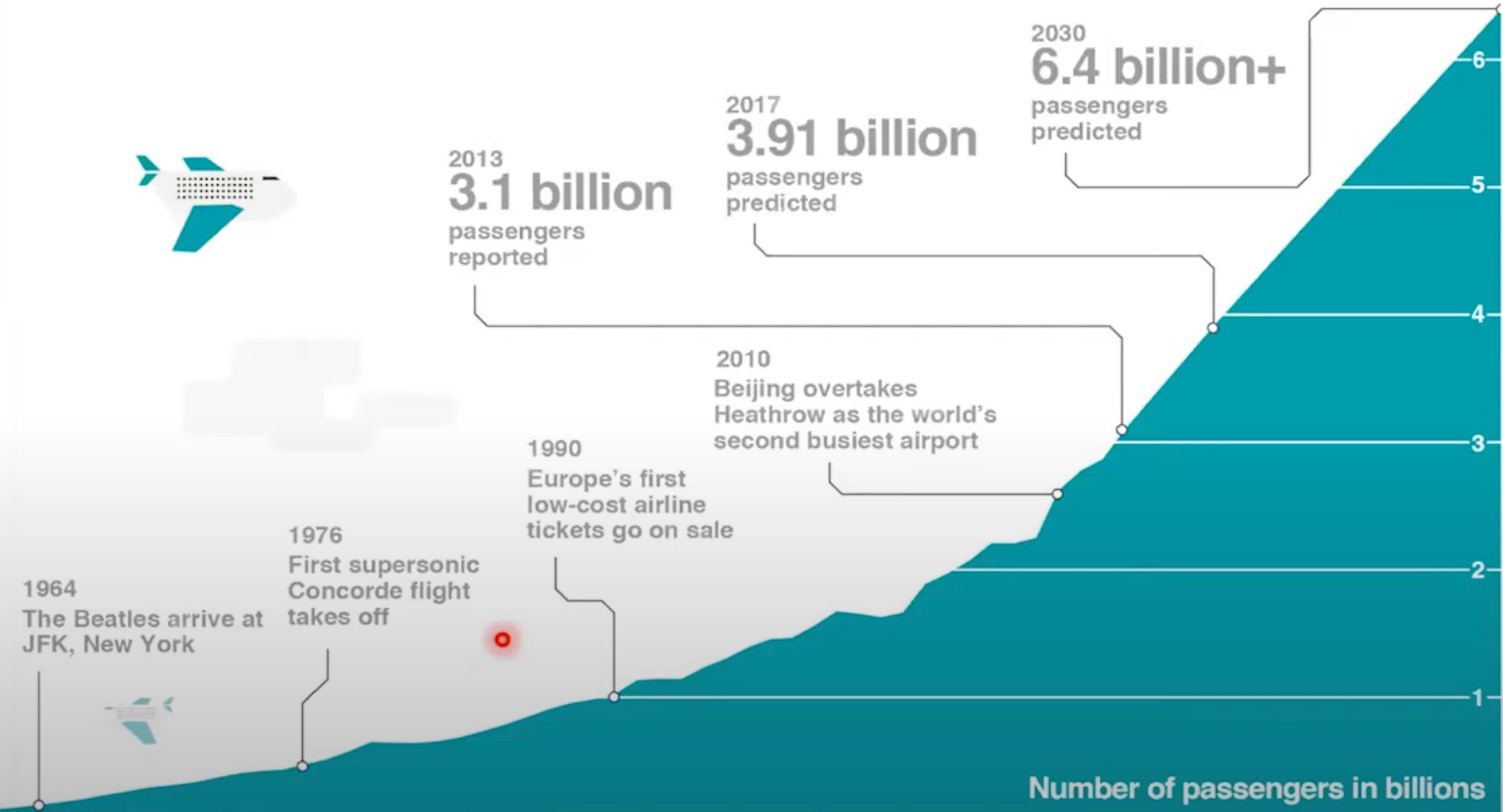
2013
3.1 billion
passengers
reported

2017
3.91 billion
passengers
predicted

2010
Beijing overtakes
Heathrow as the world's
second busiest airport

2030
6.4 billion+
passengers
predicted

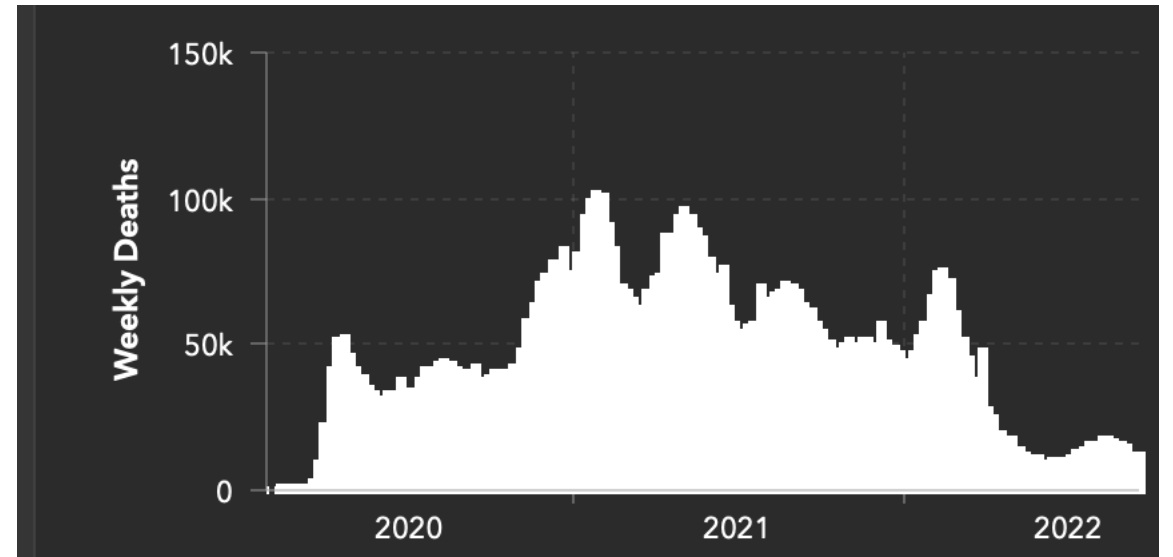
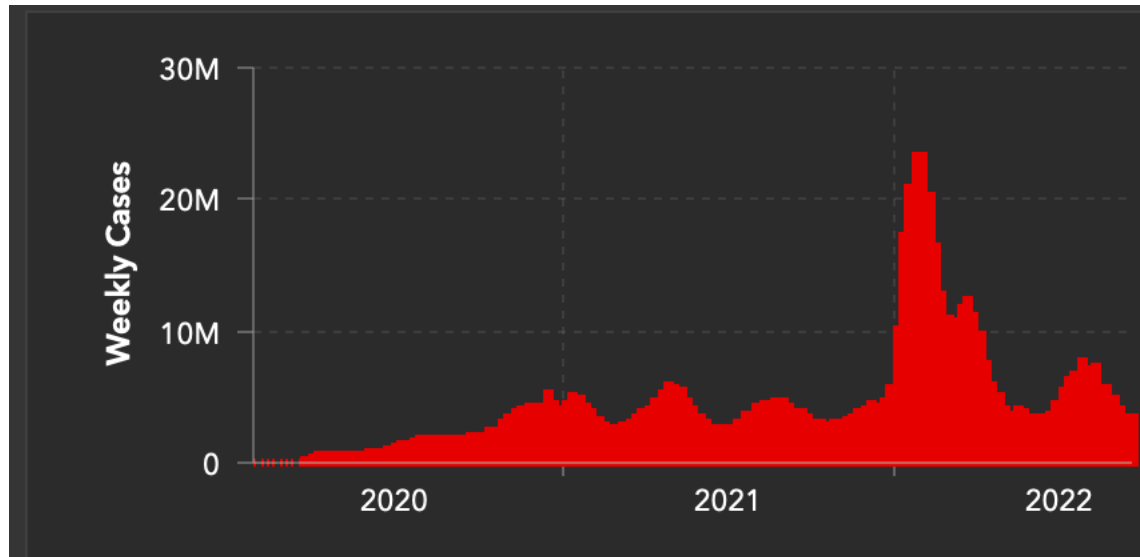
Number of passengers in billions



Infección emergente → Interacciones complejas



Ondas epidémicas durante la Pandemia de COVID-19



<https://coronavirus.jhu.edu/map.html>

Sucesivas ondas epidémicas relacionadas con la emergencia de variantes del SARS-CoV-2

Virus gripales → la gran amenaza

N ENGL J MED 350;3 WWW.NEJM.ORG JANUARY 15, 2004

PERSPECTIVE

Influenza Vaccine — Outmaneuvering Antigenic Shift and Drift

Influenza Vaccine — Outmaneuvering Antigenic Shift and Drift

John Treanor, M.D.

Los cambios antigénicos mayores (Shift) y menores (Drift) en la hemaglutinina y neuraminidasa en virus gripales provocan epidemias de gripe estacional y pandemias

¿Cambió el virus Zika?



Molecular Evolution of Zika Virus during Its Emergence in the 20th Century

Oumar Faye¹*, Caio C. M. Freire²*, Atila Iamarino², Ousmane Faye¹, Juliana Velasco C. de Oliveira², Mawlouth Diallo¹, Paolo M. A. Zanotto², Amadou Alpha Sall^{1*}

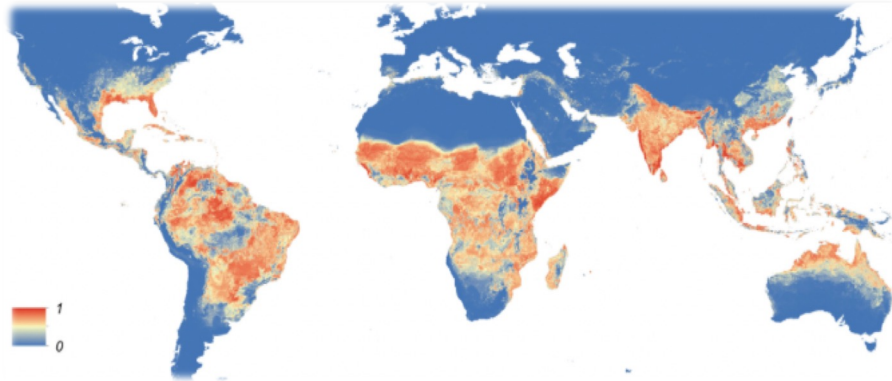
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Abstract

Zika virus (ZIKV) is a mosquito-borne flavivirus first isolated in Uganda in 1947. Although entomological and virologic surveillance have reported ZIKV enzootic activity in diverse countries of Africa and Asia, few human cases were reported until 2007, when a Zika fever epidemic took place in Micronesia. In the context of West Africa, the WHO Collaborating Centre for Arboviruses and Hemorrhagic Fever at Institut Pasteur of Dakar (<http://www.pasteur.fr/recherche/banques/CRORA/>) reports the periodic circulation of ZIKV since 1968. Despite several reports on ZIKV, the genetic relationships among viral strains from West Africa remain poorly understood. To evaluate the viral spread and its molecular epidemiology, we investigated 37 ZIKV isolates collected from 1968 to 2002 in six localities in Senegal and Côte d'Ivoire. In addition, we included strains from six other countries. Our results suggested that these two countries in West Africa experienced at least two independent introductions of ZIKV during the 20th century, and that apparently these viral lineages were not restricted by mosquito vector species. **Moreover, we present evidence that ZIKV has possibly undergone recombination in nature and that a loss of the N154 glycosylation site in the envelope protein was a possible adaptive response to the *Aedes dalzieli* vector.**

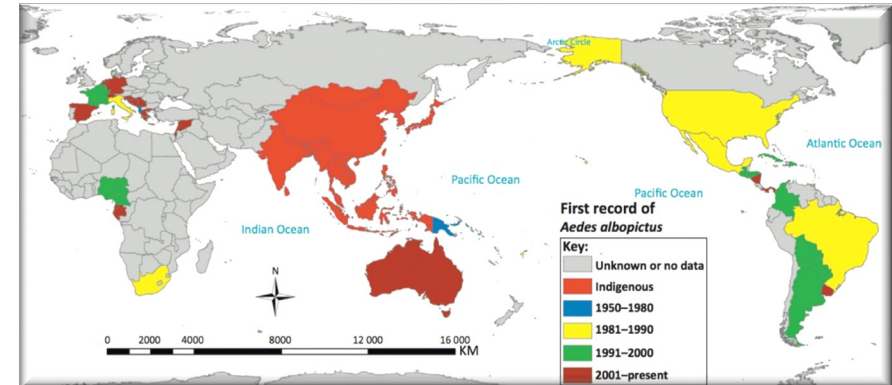
En su evolución, la recombinación entre virus y la pérdida de genes dio lugar a un virus más infectivo y mejor adaptado a los vectores

Amplia y rápida expansión de vectores



Aedes aegypti

Origen africano
Amplia distribución por Asia,
Oceanía y Américas



Aedes albopictus

Origen en sudeste asiático
Amplia y rápida distribución
mundial

Artrópodos vectores → la otra amenaza

- Transmiten bacterias, virus, protozoos, nematodos, toxinas.
- Gran morbimortalidad - Responsables del 17% de toda la carga que suponen las enfermedades infecciosas.

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- Gran morbimortalidad - Responsables del 17% de toda la carga que suponen las enfermedades infecciosas.

La OMS estimó que en 2020 se produjeron 241 millones de afectados por Paludismo y 627.000 muertes.

Se estima (OMS) que la mitad de la población mundial se encuentra en riesgo de infectarse por el virus del dengue, con 390 millones de infectados al año y alrededor de 40.000 muertes.

Los CDC y ECDC estiman ≈ 500.000 casos de b. de Lyme anuales en EEUU-Europa.

Gran número de infecciones emergentes asociadas, producción de brotes y epidemias (Zika, fiebre amarilla, Oeste del Nilo, encefalitis japonesa, Crimea-Congo, TBE, síndrome de la trombocitopenia severa febril, virus Bourbon...)



(GIGA)byte

DATA RELEASE

AIMSurv: First pan-European harmonized surveillance of *Aedes* invasive mosquito species of relevance for human vector-borne diseases

Miguel Ángel Miranda^{1,*}, Carlos Barceló¹, Daniele Arnoldi², Xenia Augsten³, Karin Bakran-Lebl⁴, George Balatsos⁵, Mikel Bengoa⁶, Philippe Bindler⁷, Kristina Boršová⁸, Maria Bourquia⁹, Daniel Bravo-Barriga¹⁰, Viktória Čabanová⁸, Beniamino Caputo¹¹, Maria Christou¹², Sarah Delacour¹³, Roger Eritja¹⁴, Ouafaa Fassi-Fihri⁹, Martina Ferraguti¹⁵, Eleonora Flacio¹⁶, Eva Frontera¹⁰, Hans Peter Fuehrer¹⁷, Ana L. García-Pérez¹⁸, Pantelis Georgiades¹², Sandra Gewehr¹⁹, Fátima Goiri¹⁸, Mikel Alexander González²⁰, Martin Gschwind²¹, Rafael Gutiérrez-López¹, Cintia Horváth²², Adolfo Ibáñez-Justicia²³, Viola Jani²⁴, Përparim Kadriaj²⁴, Katja Kalan²⁵, Mihaela Kavran²⁶, Ana Klobucar²⁷, Kornélia Kurucz²⁸, Javier Lucientes¹³, Renke Lühken²⁹, Sergio Magallanes¹⁵, Giovanni Marini², Angeliki F. Martinou³⁰, Alice Michelutti³¹, Andrei Daniel Mihalca²², Tomás Montalvo³², Fabrizio Montarsi³¹, Spiros Mourelatos¹⁹, Nesade Muja-Bajraktari³³, Pie Müller²¹, Gregoris Notarides³⁴, Hugo Costa Osório³⁵, José A. Oteo³⁶, Kerem Oter³⁷, Igor Pajović³⁸, John R. B. Palmer³⁹, Suncica Petrinic²⁷, Cristian Răileanu⁴⁰, Christian Ries⁴¹, Elton Rogozi²⁴, Ignacio Ruiz-Arrondo³⁶, Isis Sanpera-Calbet³⁹, Nebojša Sekulić⁴², Kivanc Sevim⁴³, Kurtesh Sherifi⁴⁴, Cornelia Silaghi⁴⁰, Manuel Silva³⁵, Nikolina Sokolovska⁴⁵, Zoltán Soltész⁴⁶, Tatiana Sulesco⁴⁷, Jana Šušnjar²⁵, Steffanie Teekema²³, Andrea Valsecchi³², Marlen Ines Vasquez³⁴, Enkelejda Velo²⁴, Antonios Michaelakis⁵, William Wint⁴⁸, Dušan Petrić²⁶, Francis Schaffner⁴⁹, Alessandra della Torre¹¹ and Consortium AIM-COST/AIM-Surv[†]

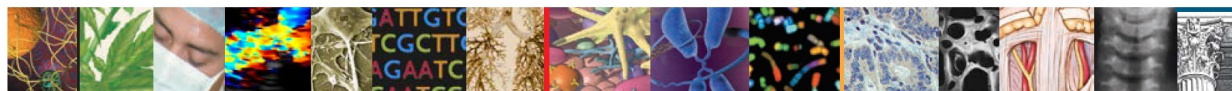
Submitted: 23 March 2022
Accepted: 19 May 2022
Published: 23 May 2022

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<https://ipt.gbif.es/resource?r=aimsurv>

Gran expansión y adaptación del *Aedes albopictus* (mosquito tigre) por Europa



The NEW ENGLAND JOURNAL of MEDICINE

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Perspective

Preventive Medicine for the Planet and Its Peoples

David J. Hunter, M.B., B.S., Sc.D., Howard Frumkin, M.D., Dr.P.H., and Ashish Jha, M.D., M.P.H.

“Health is the human face of climate change” was the motivating idea behind the Climate and Health conference held at the Carter Center in Atlanta on Thursday, February 16, 2017.

within the lifetimes of children now being born. What do these changes mean for health?

With warming temperatures come longer summer heat waves that increase mortality, particular-

The distribution of vectorborne diseases such as Lyme disease, West Nile virus, Rocky Mountain spotted fever, plague, and tularemia expands as the range of their vectors changes. The distribution of the Lyme disease tick, *Ixodes scapularis*, for instance, is projected to expand to cover most of the eastern half of the United States over the next 60 years.³ The mosquito vectors of pathogens not currently common in the United States, such as dengue, chikungunya, and Zika, may find more favorable conditions.

La distribución de las enfermedades transmitidas por vectores se expanden en el rango que lo hacen los artrópodos

Resistencia de *Aedes albopictus* a Piretroides

Pichler et al. *Parasites & Vectors* (2022) 15:280
<https://doi.org/10.1186/s13071-022-05407-3>

Parasites & Vectors

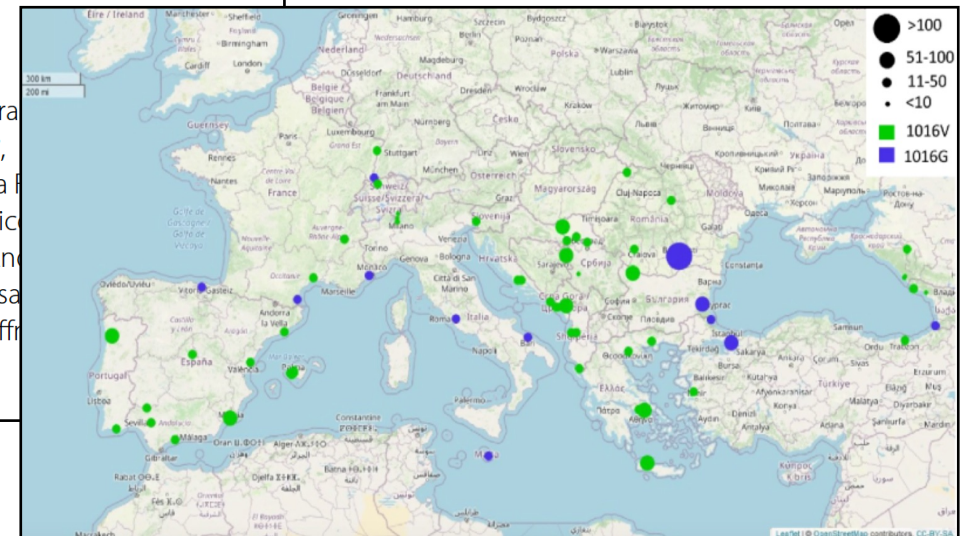
BRIEF REPORT

Open Access



Geographic distribution of the V1016G knockdown resistance mutation in *Aedes albopictus*: a warning bell for Europe

Verena Pichler^{1†}, Beniamino Caputo^{1†}, Vera Valadas^{2†}, Martina Micocci¹, Cintia Horvath³, Chiara Mustafa Akiner⁴, Georgios Balatsos⁵, Christelle Bender⁶, Gilles Besnard⁷, Daniel Bravo-Barriga⁸, Rubén Bueno-Mari⁹, Francisco Collantes¹⁰, Sarah Delacour-Estrella¹¹, Enkelejda Dikolli¹², Elena Eleonora Flacio¹⁴, Ana L. García-Pérez¹⁵, Katja Kalan¹⁶, Mihaela Kavran¹⁷, Gregory L'Ambert⁷, Ricardo Eduardo Marabuto¹⁹, Raquel Medialdea²⁰, Rosario Melero-Alcibar²¹, Antonios Michaelakis⁵, An Ognyan Mikov²², Miguel A. Miranda²³, Pie Müller^{24,25}, Domenico Otranto¹⁸, Igor Pajovic²⁶, Dusa Maria Teresa Rebelo²⁷, Vincent Robert²⁸, Elton Rogozi¹², Ana Tello²¹, Toni Zitko²⁹, Francis Schaffner Joao Pinto² and Alessandra della Torre^{1*}



Amplia distribución de genes que confieren resistencia a Piretroides (adulticidas) en Europa

Presencia especies invasivas de dípteros en Europa

An emerging threat

Mosquito-borne diseases in Europe

ECDC
EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

Mosquitoes can carry infectious diseases from person to person and from place to place.

Tropical mosquito-borne diseases are originally prevalent in tropical and subtropical regions. Some are especially endemic in regions of Africa, Asia, and the Americas and cause substantial illness for more than one billion people globally.

An emerging (or re-emerging) infectious disease is often a disease already known but spreading to new geographic areas, new populations, or reappearing after having been eradicated.

Just one bite away from infection

Different species of mosquitos can carry different diseases

Invasive mosquitos are determined by their ability to colonise new territories. A considerable increase in the spread of invasive mosquitos has been observed in Europe since the late 1990s.

1. After dispearence in the 20th century *Aedes aegypti* has recently established in Madeira. It is also present around the Black Sea coast, Russia and Georgia.

2. *Aedes albopictus* is considered to be the most invasive mosquito species in the world.

3. *Culex pipiens* is the most widespread mosquito in Europe.

4. The *Anopheles* mosquito can be found from south-eastern Sweden to Portugal.

Invasive mosquitos (1, 2)

local mosquitos (3, 4)

A **West Nile Fever**
Cases can be severe, most often among the elderly. An estimated 1 out of 140 to 320 persons infected can get severely sick.

B **Dengue:**
Most infected people have fever lasting 10 days. More than 390 million cases are estimated worldwide.

C **Chikungunya**
Infected people suffer from fever and strong arthralgia, which can last for months. No vaccination is available.

D **Malaria**
Worldwide, approx. 600 000 deaths people die every year. Early diagnosis and prompt treatment can prevent illness and death. Prophylaxis is available.

Alto riesgo de brotes epidémicos/epidemias de dengue, Chikungunya, Zika
Posibilidad de re-emergencia de la Malaria en Europa (*Anopheles* spp. + Viajeros)

Amenaza de arbovirosis emergentes transmitidas por dípteros en España

Familia / género	Virus	Vectores	Reservorios
<i>Flaviviridae / Flavivirus</i>	OESTE NILO	<i>Culex spp</i>	Aves
	DENGUE	<i>Ae. aegypti, Ae. albopictus</i>	Humanos, otros primates
	ZIKA	<i>Ae. aegypti, Ae. albopictus</i>	Humanos, mamíferos
	Fiebre amarilla	<i>Ae. aegypti, Ae. africanus, Haemagogus spp</i>	Monos, humanos
	Encefalitis Japonesa	<i>Culex spp, Aedes spp</i>	Aves acuáticas, cerdos
<i>Phenuiviridae / Phlebovirus</i>	Toscana	<i>Phlebotomus spp</i>	Flebotomos
	Valle del Rift	<i>Aedes spp, Culex spp</i>	Roedores, ganado
<i>Togaviridae / Alphavirus</i>	CHIKUNGUNYA	<i>Ae. aegypti, Ae. albopictus</i>	Humanos, otros primates

Presencia especies invasivas de artrópodos vectores



¿Qué sucederá ante el incremento de especies invasivas de dípteros en una población virgen a los agentes que transmiten?

¿Y que pasa con las garrapatas?

Medlock et al. *Parasites & Vectors* 2013, 6:1
<http://www.parasitesandvectors.com/content/6/1/1>

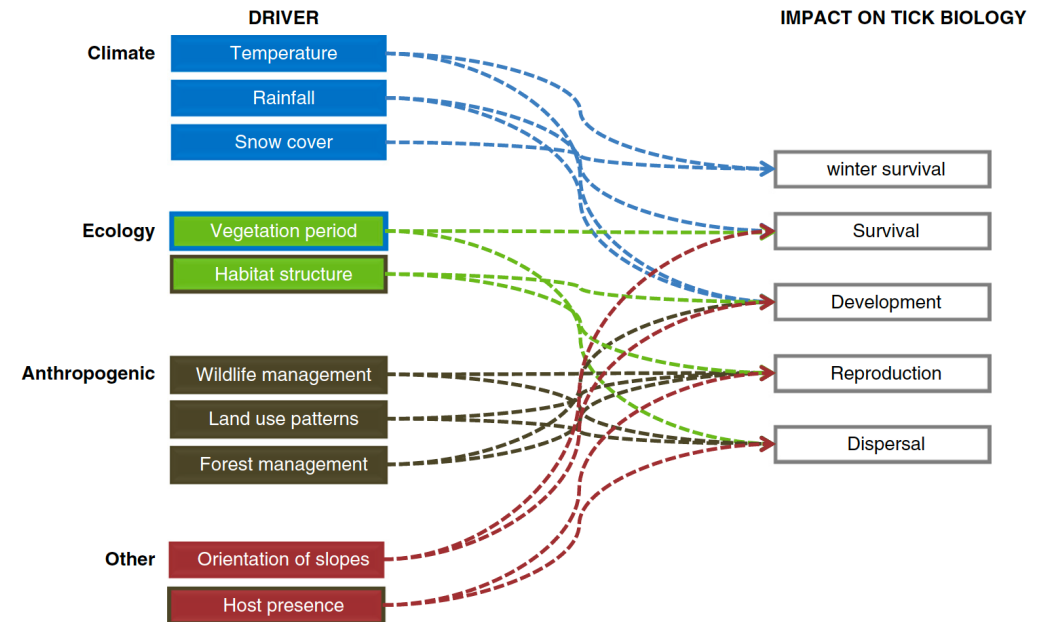


REVIEW

Open Access

Driving forces for changes in geographical distribution of *Ixodes ricinus* ticks in Europe

Jolyon M Medlock^{1*}, Kayleigh M Hansford¹, Antra Bormane², Marketa Derdakova^{3,10}, Agustín Estrada-Peña⁴, Jean-Claude George⁵, Irina Golovljova⁶, Thomas GT Jaenson⁷, Jens-Kjeld Jensen⁸, Per M Jensen⁹, Maria Kazimirova¹⁰, José A Oteo¹¹, Anna Papa¹², Kurt Pfister¹³, Olivier Plantard¹⁴, Sarah E Randolph¹⁵, Annapaola Rizzoli¹⁶, Maria Margarida Santos-Silva¹⁷, Hein Sprong¹⁸, Laurence Vial¹⁹, Guy Hendrickx²⁰, Herve Zeller²¹ and Wim Van Bortel²¹

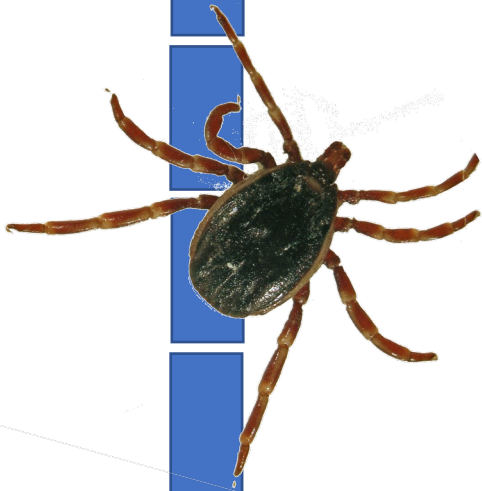


Existen diferentes factores que están modificando la abundancia y distribución de estos vectores

Emergencia de la fiebre hemorrágica de Crimea-Congo en España

2006

- ✓ Presencia del vector/reservorio y creciente número de picaduras



Incremento de las personas picadas por *Hyalomma marginatum* en La Rioja

Emergencia de la fiebre hemorrágica de Crimea-Congo en España

2006

- ✓ Presencia del vector/reservorio y creciente número de picaduras

2010

- ✓ Primera detección del virus en el sur de Europa



Cáceres



Hyalomma lusitanicum



Cervus elaphus

Crimean-Congo Hemorrhagic Fever Virus in Ticks, Southwestern Europe, 2010

To the Editor: Crimean-Congo hemorrhagic fever virus (CCHFV; family *Bunyaviridae*, genus *Nairovirus*) causes outbreaks of severe hemorrhagic fever in humans, with case-fatality rates $\leq 30\%$ (1,2). The disease was initially recognized by Russian scientists in the 1940s (3), and the virus was first isolated in the Democratic Republic of Congo some years later (4). CCHFV is reported throughout broad regions of Africa, Europe, the Middle East, and Asia. Reports linking transmission of the virus with an infected vector have involved ticks of the genus *Hyalomma* (5). It appears that maintenance of active foci of CCHFV in the field is dependent on *Hyalomma* spp., even within periods of silent activity. Several vertebrates are involved in the natural transmission cycle (6). Transmission of CCHFV to humans occurs through tick bites, direct contact with blood or tissues of infected animals, person-to-person spread, or by nosocomial infection (1).

In southeastern Europe, the Balkans are the known western limit for CCHFV (7). This finding is of special interest because *Hyalomma marginatum*, the main tick vector in the western Palearctic (an ecozone that includes temperate and cold areas of Eurasia and North Africa and several archipelagos and islands in the Atlantic and Pacific Oceans), is common throughout the Mediterranean Basin (7), where clinical cases of the disease or the virus have not been reported. Unsupported claims of the effects of climate on virus distribution have been reported but never empirically demonstrated (8).

We report the detection of CCHFV in ticks collected in southwestern

Europe. A total of 117 semi-engorged adult *H. lusitanicum* ticks were collected from 28 adult red deer (*Cervus elaphus*) in November 2010, at a site (39.63°N, 7.33°W) in Cáceres, Spain. Live ticks were transported to the special pathogens laboratory at Hospital San Pedro-CIBIR in Logroño (northern Spain), classified, and frozen at -80°C . For RNA extraction, specimens were washed in 70% ethanol and then in Milli-Q water (Milli-Q Advantage water system; Millipore Iberica, S.A., Madrid, Spain) that had been autoclaved. Each tick was cut lengthwise; half was used for additional processing and the remainder was stored. Before use, each half was crushed in sterile conditions. RNA was individually extracted by using the RNeasy Mini Kit (QIAGEN, Hilden, Germany) according to the manufacturer's instructions and frozen at -80°C .

The RNA was distributed in 12 pools and retrotranscribed by using the Omniscript RT kit (QIAGEN) according to the manufacturer's instructions and then frozen at -20°C . Nested PCRs were performed by using specific primers for the small segment of CCHFV as described (9). Negative controls (with template DNA but without primers and with primers and containing water instead of template DNA) were included in all assays.

For the second round of PCRs, 2 of 12 pools showed amplicons of the expected size (211 bp). Only 1 amplicon could be sequenced. MEGA5 (www.megasoftware.net) was used to compare the sequence with representative small segment sequences of CCHFV available in GenBank (Figure). (Aligned sequences are available from the authors.) Pools of cDNA were submitted to the Spanish National Center of Microbiology (Madrid), where results were confirmed. The CCHFV sequence we report showed 98% genetic similarity (204/209 bp) with sequences recorded for CCHFV

in Mauritania and Senegal, on the western coast of Africa.

This finding suggests the circulation of CCHFV in southwestern Europe. The close affinity of the strain from Spain with strains circulating in western Africa and the lack of similarity with isolates from eastern Europe suggest the introduction of this virus from nearby countries of northern Africa. Migratory movements of birds could explain the presence of the virus in southwestern Europe because birds are common hosts of immature *H. marginatum*, which was reportedly introduced into Europe through annual migratory flights along the western coast of Africa (10). Because of the lack of genetic similarities among virus strains, trade movements of domestic or wild ungulates from eastern Europe do not support our finding.

We cannot state whether this virus was circulating previously or if other strains are present in the area because CCHFV detection in the western Mediterranean region has not been previously addressed. *H. lusitanicum* ticks exist as relatively isolated populations in a narrow strip from Sicily to Portugal. The Mediterranean rabbit and ungulates, the main hosts for immature and adult *H. lusitanicum* ticks, respectively, are residents of the collection area; however, the movement of these animals through trade has not occurred for several years. Thus, *H. lusitanicum* ticks could not serve as a spreading vector in the western Mediterranean region. The CCHFV strain from southwestern Europe has been found in ticks restricted to hosts that cannot spread long distances. Therefore, although it would be unlikely, given the strain's similarity with CCHFV isolates from Senegal and Mauritania, we should not exclude the possibility of an ancient existence for this strain. Additional data collected in the Mediterranean Basin are necessary to establish the actual range of CCHFV.

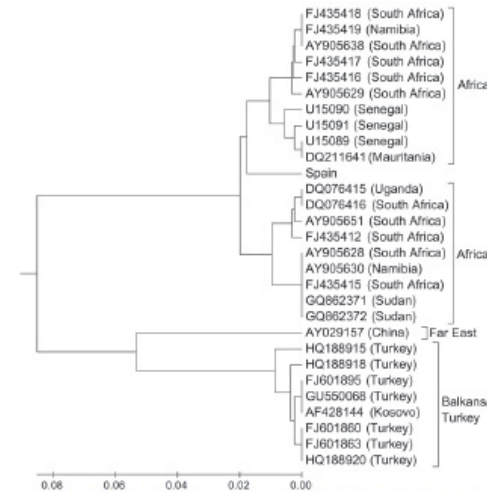


Figure. Evolutionary relationships of Crimean-Congo hemorrhagic fever virus strains from Spain and other representative sites. Evolutionary history was inferred by using the unweighted pair group method with arithmetic mean. The optimal tree is shown (sum of branch length, 0.36861921). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Evolutionary distances were computed by using the maximum composite likelihood method and are in the units of the no. of base substitutions per site. Analysis involved 29-nt sequences. The first, second, third, and noncoding codon positions were included. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted by using MEGA5 (www.megasoftware.net).

Acknowledgment

We thank Aysen Gargili for help with methods.

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Se describe por primera vez la presencia del vFHCC en el sur de Europa
Secuencias similares a las de Mauritania y diferentes a las Europeas

Emergencia de la fiebre hemorrágica de Crimea-Congo en España

2006

✓ Presencia del vector/reservorio y creciente número de picaduras

2010

✓ Primera detección del virus

2016

✓ Primeros casos de enfermedad

The screenshot shows the website of the Spanish Ministry of Health, Servicios Sociales e Igualdad, dated September 1, 2016. The page features a navigation menu with categories like 'Organización Institucional', 'Ciudadanos', and 'Profesionales'. The main content area is titled 'Notas de Prensa' and contains a press release titled 'Confirmados dos casos de fiebre hemorrágica de Crimea-Congo en España'. The text of the press release states: '1 de septiembre de 2016. El Centro Nacional de Microbiología del Instituto de Salud Carlos III ha confirmado dos casos de fiebre hemorrágica de Crimea-Congo, los primeros diagnosticados en España. El primer caso es el de un paciente, ya fallecido, que fue atendido en un hospital de la Comunidad de Madrid. El segundo caso se trata de una mujer enfermera de la UCI que atendió a este mismo paciente.' It also mentions the ministry's collaboration with the Madrid community and the activation of the national protocol for the disease.

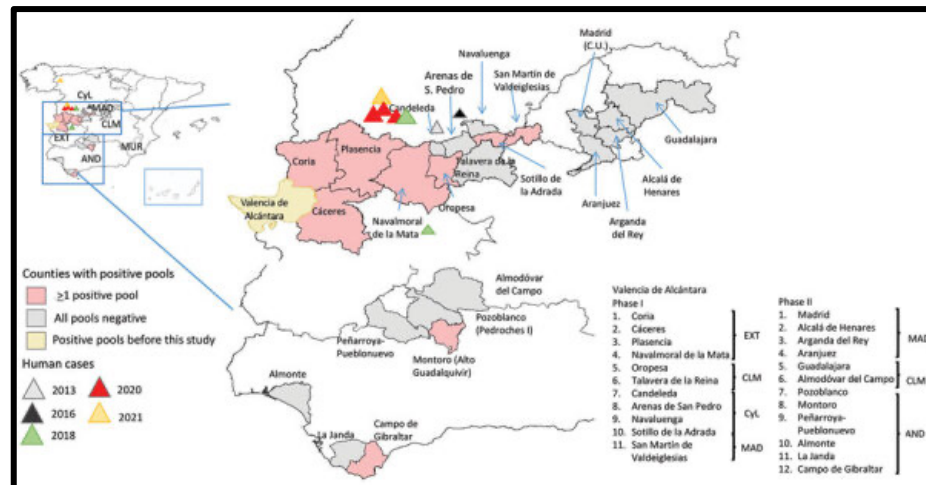
RESEARCH LETTERS

Retrospective Identification of Early Autochthonous Case of Crimean-Congo Hemorrhagic Fever, Spain, 2013

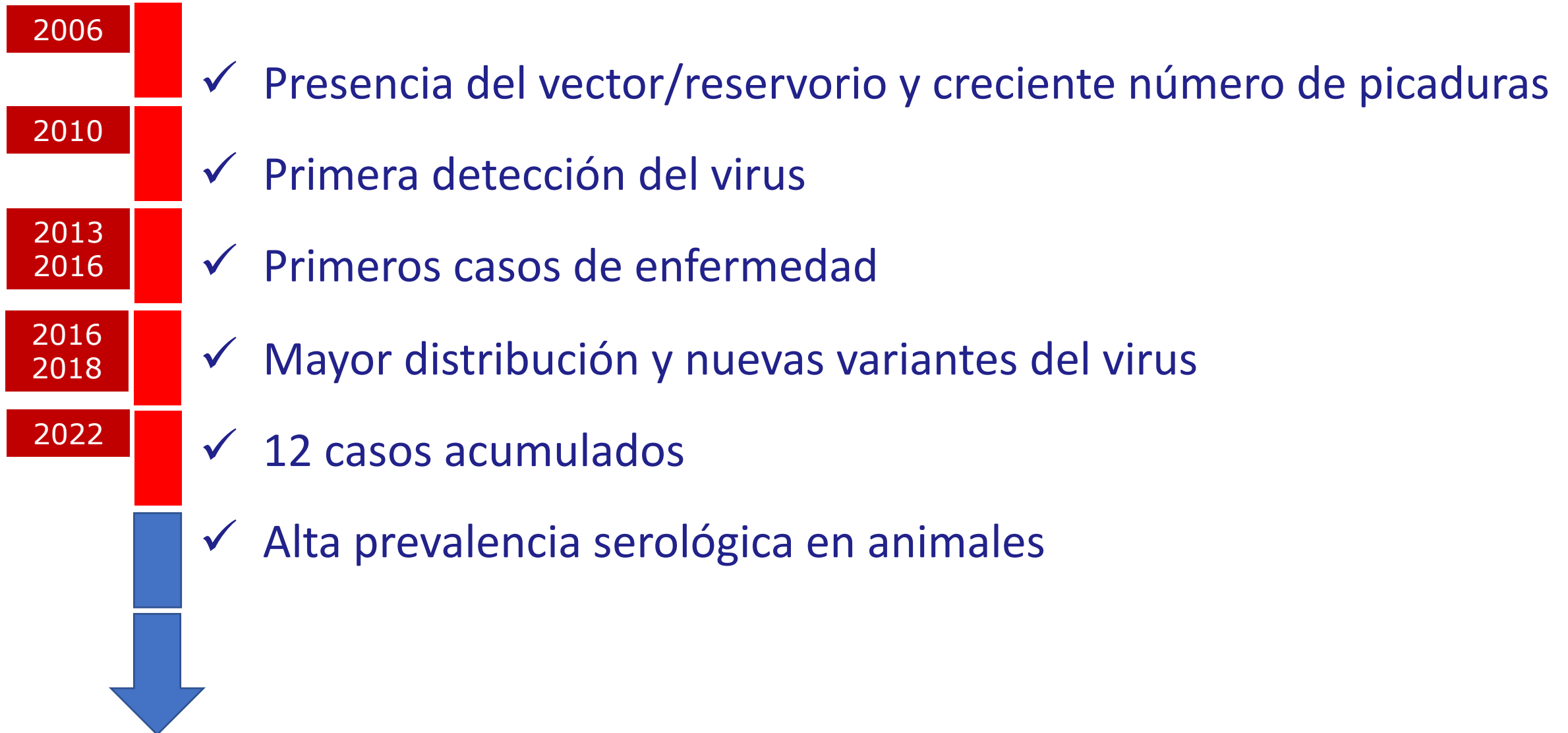
Ana Negrodo,¹ María Sánchez-Ledesma,¹ Francisco Llorente, Mayte Pérez-Olmeda, Moncef Belhassen-García, David González-Calle, María Paz Sánchez-Seco,² Miguel Ángel Jiménez-Clavero²

Emergencia de la fiebre hemorrágica de Crimea-Congo en España

- 2006 ✓ Presencia del vector/reservorio y creciente número de picaduras
- 2010 ✓ Primera detección del virus
- 2013
2016 ✓ Primeros casos de enfermedad
- 2016
2018 ✓ Mayor distribución y nuevas variantes del virus



Emergencia de la fiebre hemorrágica de Crimea-Congo en España





Cortesía de Carlos Pradera

Microorganisms **2021**, *9*, 649. <https://doi.org/10.3390/microorganisms9030649>



microorganisms



Review

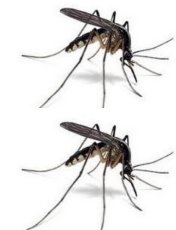
Epidemiological Aspects of Crimean-Congo Hemorrhagic Fever in Western Europe: What about the Future?

Aránzazu Portillo , Ana M. Palomar , Paula Santibáñez and José A. Oteo *

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8003855/pdf/microorganisms-09-00649.pdf>

Infecciones que necesitaban ser investigadas por su potencial epidémico

- **Fiebre hemorrágica de Crimea-Congo**
- Enfermedad por virus Ébola y Marburg
- Fiebre de Lassa
- MERS y SARS coronavirus
- Enfermedad por virus Nipah y Henipa
- Fiebre del Valle de Rift
- Enfermedad por virus Zika
- **Enfermedad X**



¿Qué sucede con las especies de garrapatas invasivas?

2017

Journal of Medical Entomology, 55(3), 2018, 757–759
doi: 10.1093/jme/tjy006
Advance Access Publication Date: 19 February 2018
Short Communication

Discovery of *Haemaphysalis longicornis* (Ixodida: Ixodidae) Parasitizing a Sheep in New Jersey, United States

Tadhg Rainey,¹ James L. Occi,² Richard G. Robbins,³ and Andrea Egizi^{2,4,5}

¹Hunterdon County Division of Health, Flemington, NJ 08822-2900, ²Center for Vector Biology, Department of Entomology, Rutgers University, New Brunswick, NJ 08901-8536, ³Walter Reed Biosystematics Unit, Department of Entomology, Smithsonian Institution, Suitland, MD 20746-2863, ⁴Tick-borne Diseases Laboratory, Monmouth County Mosquito Control Division NJ 08901-8536, and ⁵Corresponding author: e-mail: andrea.egizi@co.monmouth.nj.us

Subject Editor: Howard Ginsberg

Received 8 December 2017; Editorial decision 3 January 2018

2018

Morbidity and Mortality Weekly Report

Multistate Infestation with the Exotic Disease–Vector Tick *Haemaphysalis longicornis* — United States, August 2017–September 2018

C. Ben Beard, PhD¹; James Occi, MA, MS²; Denise L. Bonilla, MS³; Andrea M. Egizi, PhD⁴; Dina M. Fonseca, PhD²; James W. Mertins, PhD³; Bryon P. Backenson, MS⁵; Waheed I. Bajwa, PhD⁶; Alexis M. Barbarin, PhD⁷; Matthew A. Bertone, PhD⁸; Justin Brown, DVM, PhD⁹; Neeta P. Connally, PhD¹⁰; Nancy D. Connell, PhD¹¹; Rebecca J. Eisen, PhD¹; Richard C. Falco, PhD⁵; Angela M. James, PhD³; Rayda K. Krell, PhD¹⁰; Kevin Lahmers, DVM, PhD¹²; Nicole Lewis, DVM¹³; Susan E. Little, DVM, PhD¹⁴; Michael Neault, DVM¹⁵; Adalberto A. Pérez de León, DVM, PhD¹⁶; Adam R. Randall, PhD¹⁷; Mark G. Ruder, DVM, PhD¹⁸; Meriam N. Saleh, PhD¹⁴; Brittany L. Schappach¹⁰; Betsy A. Schroeder, DVM¹⁹; Leslie L. Seraphin, DVM³; Morgan Wehtje, PhD³; Gary P. Wormser, MD²⁰; Michael J. Yabsley, PhD²¹; William Halperin, MD, DrPH²²

MMWR / November 30, 2018 / Vol. 67 / No. 47

US Department of Health and Human Services/Centers for Disease Control and Prevention



Article

Pathogen Spillover to an Invasive Tick Species: First Detection of Bourbon Virus in *Haemaphysalis longicornis* in the United States

Alexandra N. Cumbie^{1,*}, Rebecca N. Trimble² and Gillian Eastwood^{1,3,4,*}

2022



Infecciones que necesitaban ser investigadas por su potencial epidémico

- Otras fiebres hemorrágicas por Arenavirus
- Chikungunya
- Otros coronavirus diferentes que MERS y SARS
- Enterovirus no poliomiélicos (EV71, D68)
- **Síndrome de trombocitopenia severa febril**



Infección emergente → Interacciones complejas



ACUERDO DE PARÍS

- **2015:** con el objeto de combatir el cambio climático, y adaptarse a sus efectos, los Países se unieron en un acuerdo ambicioso y vinculante por primera vez.
- **Limitar el calentamiento mundial para 2050** por debajo de 2° (preferiblemente a 1,5° C) en comparación con los niveles preindustriales, mediante la disminución de las emisiones de gases con efecto invernadero.



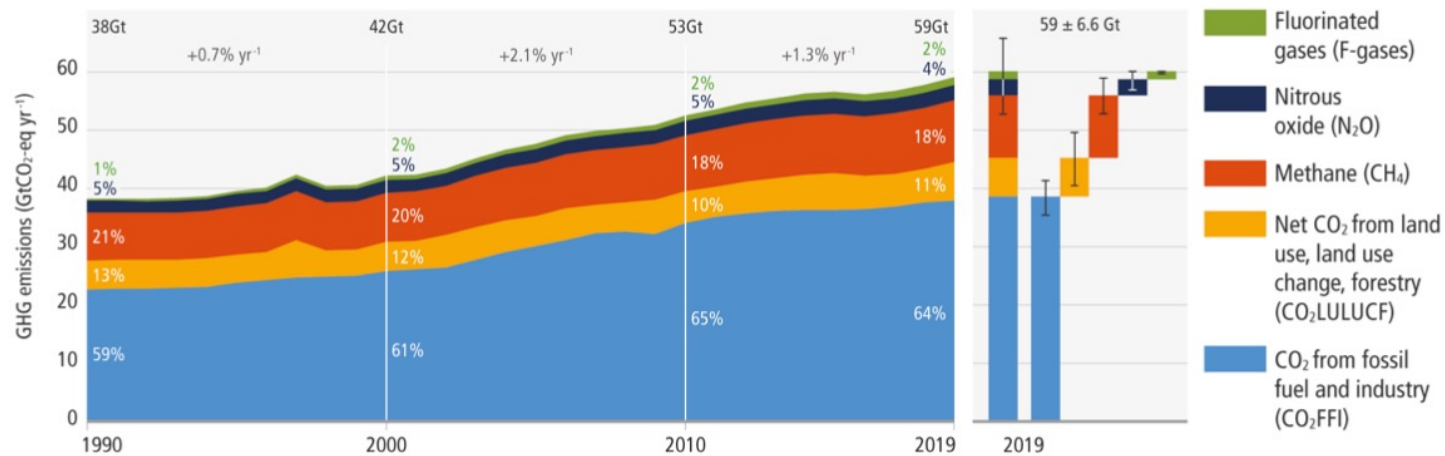
NACIONES UNIDAS
2015

Climate Change 2022

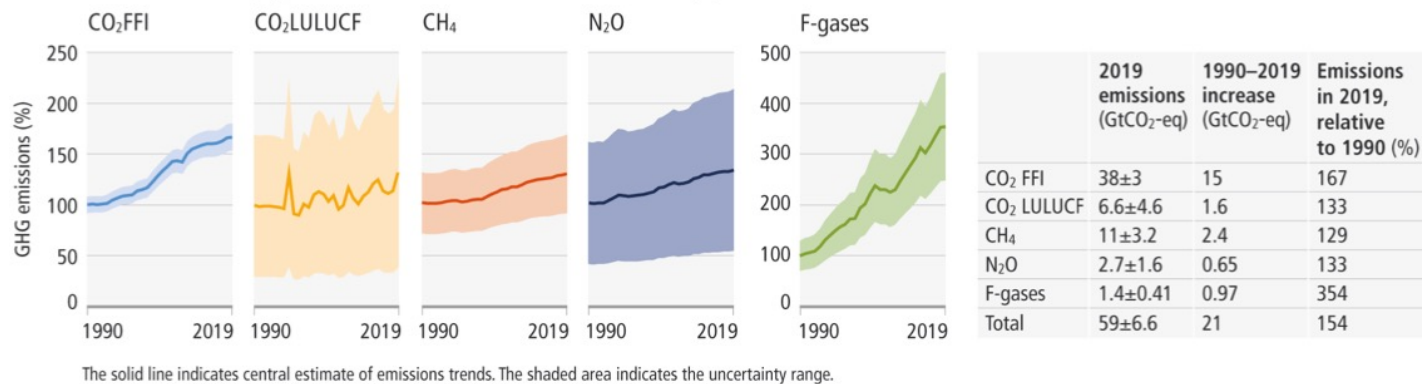
Mitigation of Climate Change



a. Global net anthropogenic GHG emissions 1990–2019 ⁽⁶⁾



b. Global anthropogenic GHG emissions and uncertainties by gas – relative to 1990

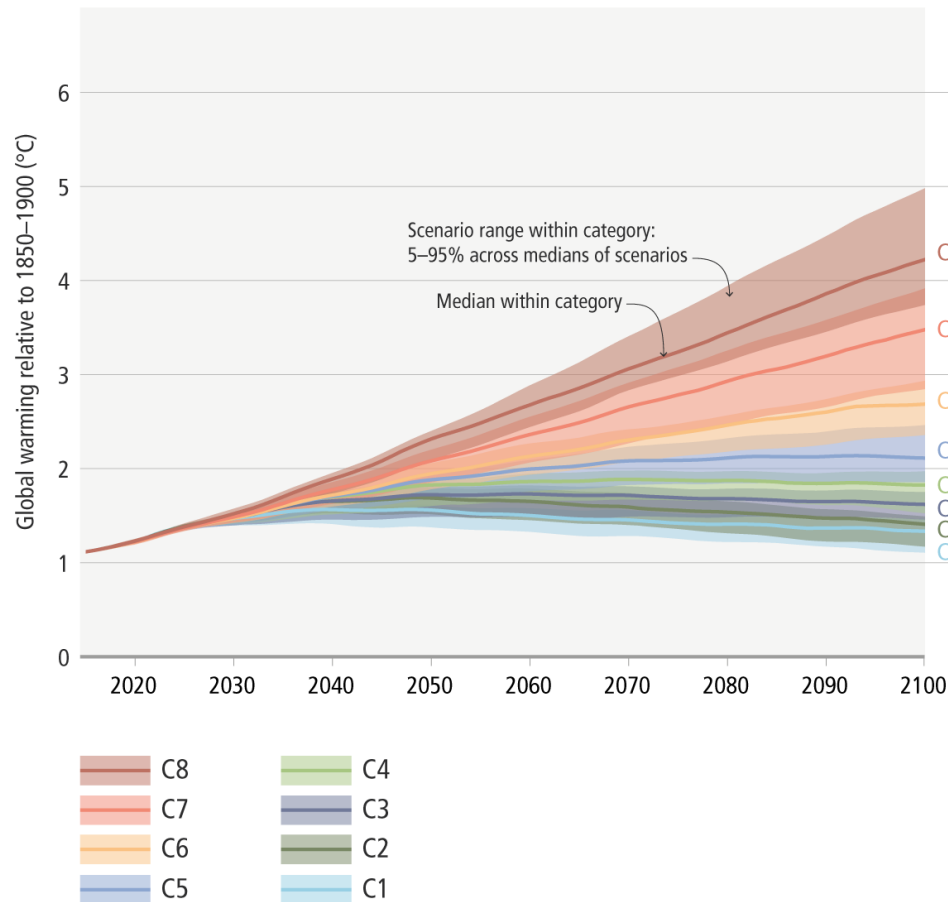


Las emisiones antroponérgicas globales netas han seguido aumentando en todos los principales grupos de gases de efecto invernadero

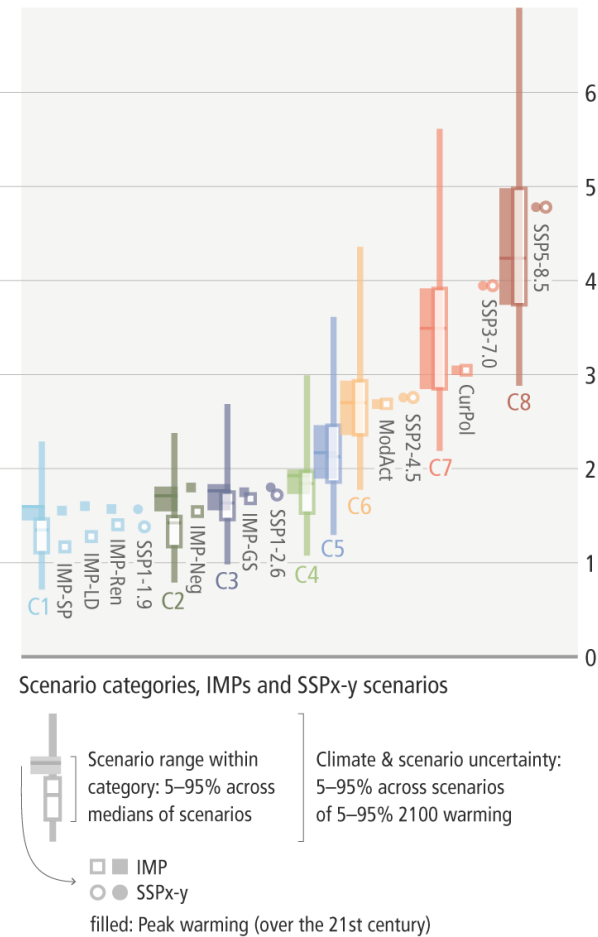
Rangos de calentamiento global para el siglo XXI

https://report.ipcc.ch/ar6wg3/pdf/IPCC_AR6_WGIII_FinalDraft_FullReport.pdf

a. Median global warming across scenarios in categories C1 to C8



b. Peak and 2100 global warming across scenario categories, IMPs and SSPx-y scenarios considered by AR6 WG1



Algunas predicciones nos sitúan en escenarios muy peligrosos para la salud

nature

<https://doi.org/10.1038/s41586-022-04788-w>

Accelerated Article Preview

Climate change increases cross-species viral transmission risk

Received: 24 January 2020

Accepted: 21 April 2022

Accelerated Article Preview

Published online: 28 April 2022

Cite this article as: Carlson, C. J. et al.
Climate change increases cross-species
viral transmission risk. *Nature*
<https://doi.org/10.1038/s41586-022-04788-w>
(2022)

Colin J. Carlson, Gregory F. Albery, Cory Merow, Christopher H. Trisos, Casey M. Zipfel,
Evan A. Eskew, Kevin J. Olival, Noam Ross & Shweta Bansal

Existen 10.000 virus capaces de infectar a humanos (la mayoría silentes en sus reservorios)

El calentamiento y los nuevos usos de la tierra propiciarán desplazamientos de animales
y nuevas interacciones entre animales y de animales con personas

Estos factores podrían facilitar el salto de especies (*spillover*) y emergencia de nuevas enfermedades

Accelerated Article Preview

Climate change increases cross-species viral transmission risk

Received: 24 January 2020

Accepted: 21 April 2022

Accelerated Article Preview

Published online: 28 April 2022

Cite this article as: Carlson, C. J. et al.

Climate change increases cross-species viral transmission risk. *Nature*

<https://doi.org/10.1038/s41586-022-04788-w>
(2022)

Colin J. Carlson, Gregory F. Albery, Cory Merow, Christopher H. Trisos, Casev M. Zipfel, Evan A. Eskew, Kevin J. Olival, Noam Ross & Shweta Bansal

Utilizan un modelo filogeográfico de proyección futura para 2070 en el escenario de cambio climático

Aumentarán las probabilidades de transmisión hasta 4.000 veces en áreas de alta densidad humana → sobre todo en África y Asia

Cambio Climático y emergencia de SARS-CoV



ELSEVIER

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv



Short Communication

Shifts in global bat diversity suggest a possible role of climate change in the emergence of SARS-CoV-1 and SARS-CoV-2

Robert M. Beyer ^{a,b,*}, Andrea Manica ^a, Camilo Mora ^c

^a Department of Zoology, University of Cambridge, Downing Street, Cambridge CB2 3EJ, United Kingdom

^b Potsdam Institute for Climate Impact Research, Telegrafenberg A 31, 14473 Potsdam, Germany

^c Department of Geography and Environment, University of Hawai'i at Manoa, 2424 Maile Way, Honolulu, HI 96822, USA

HIGHLIGHTS

- Bats are the likely zoonotic origin of SARS-CoV-1 and SARS-CoV-2.
- The local number of coronaviruses is correlated with bat species richness.
- Climate change has shifted the global distribution of bats.
- Bat richness has strongly increased in the likely origin of SARS-CoV-1 and 2.
- Climate change may have been an important factor in the outbreaks of the two viruses.

GRAPHICAL ABSTRACT

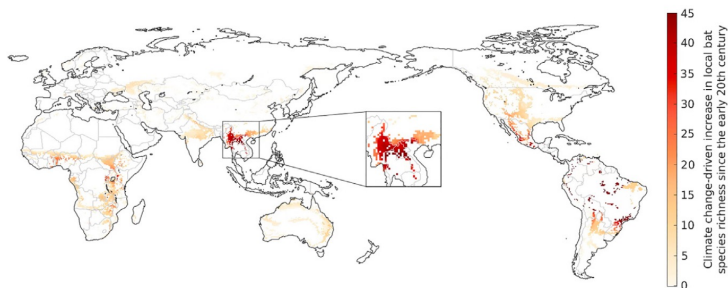
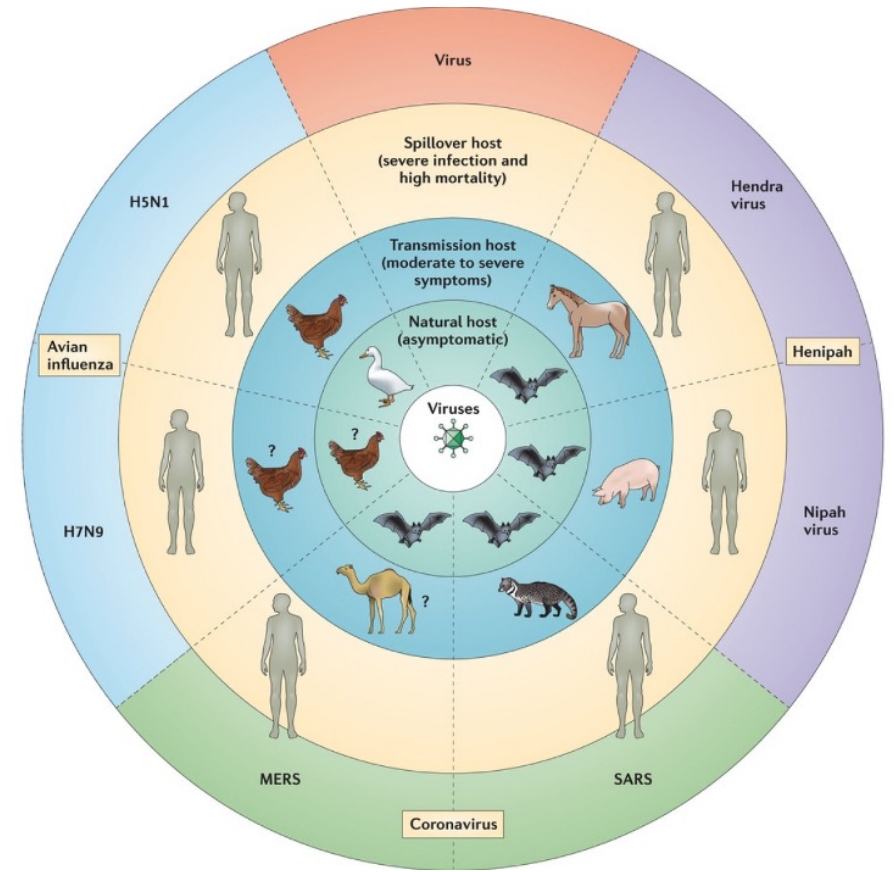


Foto: Nils Bouillard / Unsplash

Cambios en la distribución y migraciones de murciélagos como factor favorecedor del *Spillover*

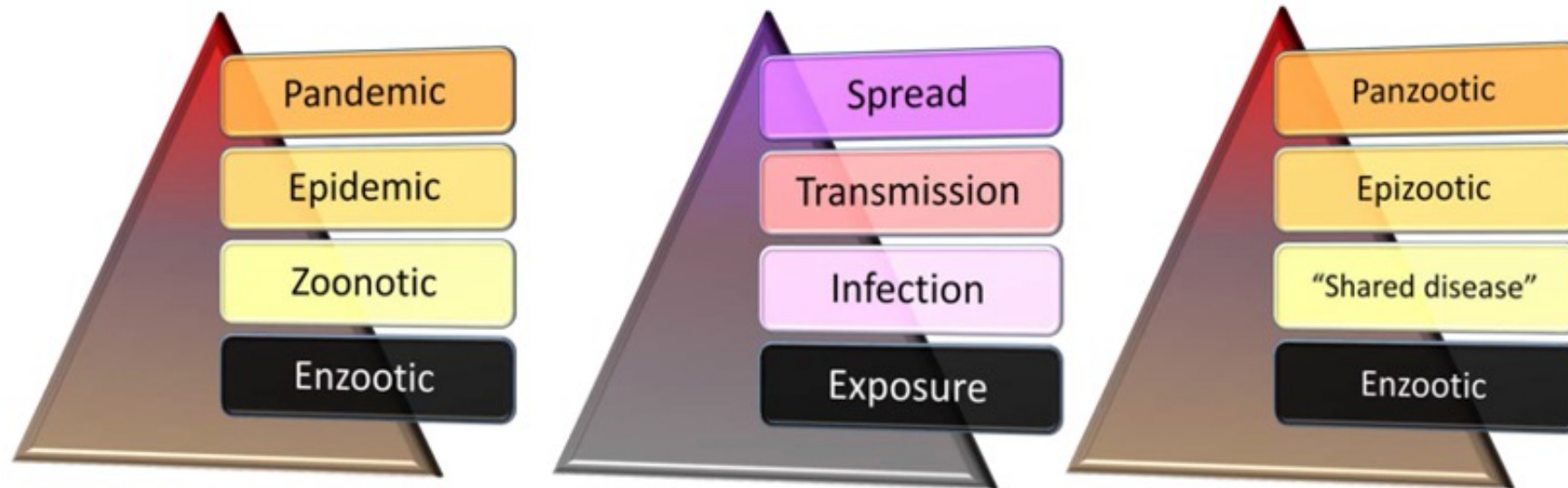
Salto de especies - *Spillover*

- Cada microorganismo puede infectar desde 1 a un amplio rango de animales (**rango de especies del patógeno**).
- La adaptación a una nueva especie es un proceso gradual basada en la **plasticidad genética del agente** que le confiere capacidad de evolucionar y de saltar la barrera entre especies.



No es un proceso fácil ni frecuente, aunque le damos continuas oportunidades

Adaptación gradual y salto de especies



Pathogen pyramid

(Adapted from Woolhouse & Gaunt, 2009)

Proceso dinámico que habitualmente se queda en el mundo animal, pero...



News > Associated Press

A Viral Reprise: When COVID-19 Strikes Again and Again

Laura Ungar

June 29, 2022

For New York musician Erica Mancini, COVID-19 made repeat performances.

March 2020. Last December. And again this May.

"I'm bummed to know that I might forever just get infected," said the 31-year-old singer, who is vaccinated and boosted. "I don't want to be getting sick every month or every 2 months."

https://www.medscape.com/viewarticle/976393?src=wnl_edit_tpal&uac=126039SG&impID=4383879&faf=1

“Yo no quiero enfermarme cada mes o dos meses a pesar de vacunarme”

Las variantes del SARS-CoV-2 nos seguirán afectando hasta que dispongamos de vacunas esterilizantes

THE WALL STREET JOURNAL.



A World Health Organization-led team investigating the origins of the Covid-19 pandemic visited the Wuhan Institute of Virology on Feb. 3.

By [Michael R. Gordon](#), [Warren P. Strobel](#) and [Drew Hinshaw](#)

May 23, 2021 2:57 pm ET

◆ WSJ NEWS EXCLUSIVE | [WORLD](#)

Intelligence on Sick Staff at Wuhan Lab Fuels Debate on Covid-19 Origin

Report says researchers went to hospital in November 2019, shortly before confirmed outbreak; adds to calls for probe of whether virus escaped lab

¿Han fallado las medidas de contención?

¿Se ha escapado de un laboratorio?

https://www.wsj.com/articles/intelligence-on-sick-staff-at-wuhan-lab-fuels-debate-on-covid-19-origin-11621796228?mod=hp_lead_pos7



[Administration](#) [Priorities](#) [COVID](#)

BRIEFING ROOM

Statement by President Joe Biden on the Investigation into the Origins of COVID-19

MAY 26, 2021 • STATEMENTS AND RELEASES

<https://www.whitehouse.gov/briefing-room/statements-releases/2021/05/26/statement-by-president-joe-biden-on-the-investigation-into-the-origins-of-covid-19/>





Soy el Dr. Virus y
aspiro a adueñarme
del mundo

I'm Dr. Evil, and I'm aspiring to
take over the world.

¿Tendremos una epidemia de COVID persistente?

Entre el 10-30% de los pacientes con COVID-19

¿Síndrome post-infeccioso?

¿Fenómeno auto-inmune inducido tras la infección?



ACC Issues Clinical Guidance on CV Consequences of COVID-19

Mar 16, 2022

ACC News Story

RESEARCH

Risks of deep vein thrombosis, pulmonary embolism, and bleeding after covid-19: nationwide self-controlled cases series and matched cohort study

Ioannis Katsoularis,¹ Osvaldo Fonseca-Rodríguez,² Paddy Farrington,³ Hanna Jerndal,² Erling Häggström Lundevaller,⁴ Malin Sund,^{5,6} Krister Lindmark,¹ Anne-Marie Fors Connolly²

BMJ 2022;376:e069590

Lancet Psychiatry 2022

Published Online

August 17, 2022

[https://doi.org/10.1016/S2215-0366\(22\)00260-7](https://doi.org/10.1016/S2215-0366(22)00260-7)

Articles

Neurological and psychiatric risk trajectories after SARS-CoV-2 infection: an analysis of 2-year retrospective cohort studies including 1 284 437 patients

Maxime Taquet, Rebecca Sillett, Lena Zhu, Jacob Mendel, Isabella Camplisson, Quentin Dercon, Paul J Harrison

Journal of Alzheimer's Disease 89 (2022) 411–414
DOI 10.3233/JAD-220717
IOS Press

411

Short Communication

Association of COVID-19 with New-Onset Alzheimer's Disease

Lindsey Wang^a, Pamela B. Davis^b, Nora D. Volkow^c, Nathan A. Berger^a, David C. Kaelber^d and Rong Xu^{e,*}

^aCenter for Science, Health, and Society, Case Western Reserve University School of Medicine, Cleveland, OH, USA

^bCenter for Community Health Integration, Case Western Reserve University School of Medicine, Cleveland, OH, USA

^cNational Institute on Drug Abuse, National Institutes of Health, Bethesda, MD, USA

^dThe Center for Clinical Informatics Research and Education, The MetroHealth System, Cleveland, OH, USA

^eCenter for Artificial Intelligence in Drug Discovery, Case Western Reserve University School of Medicine, Cleveland, OH, USA

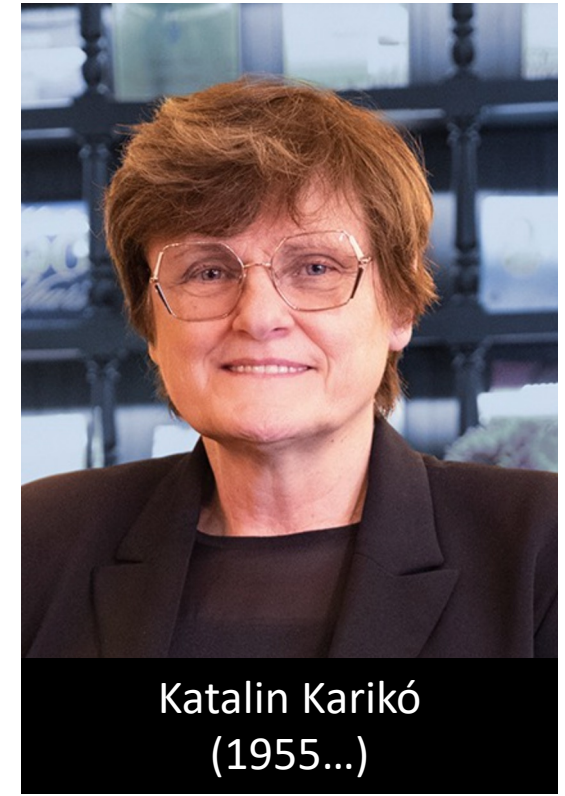
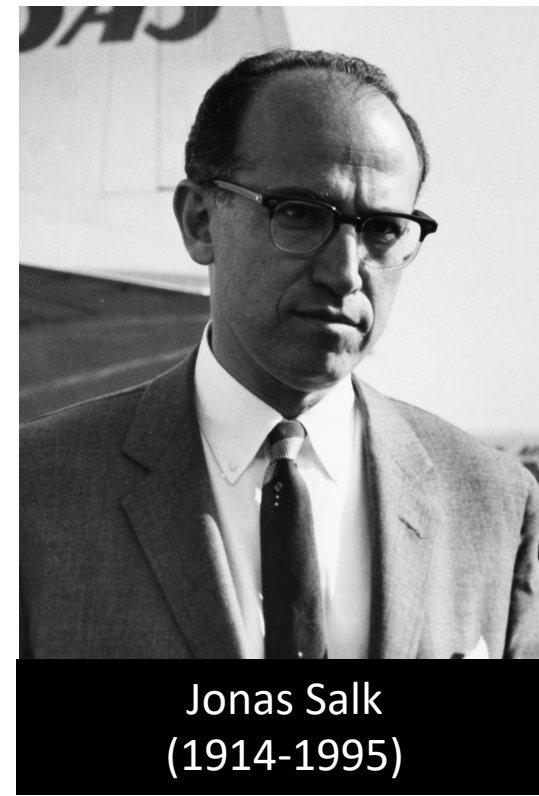
Accepted 18 July 2022
Pre-press 29 July 2022

[https://www.thelancet.com/journals/lanpsy/article/PIIS2215-0366\(22\)00260-7/fulltext](https://www.thelancet.com/journals/lanpsy/article/PIIS2215-0366(22)00260-7/fulltext)

<https://content.iospress.com/download/journal-of-alzheimers-disease/jad220717?id=journal-of-alzheimers-disease%2Fjad220717>

¿Aumentarán los casos de demencia asociada a la infección por SARs-CoV-2?

Un poco de historia: de Jenner a Karikó...

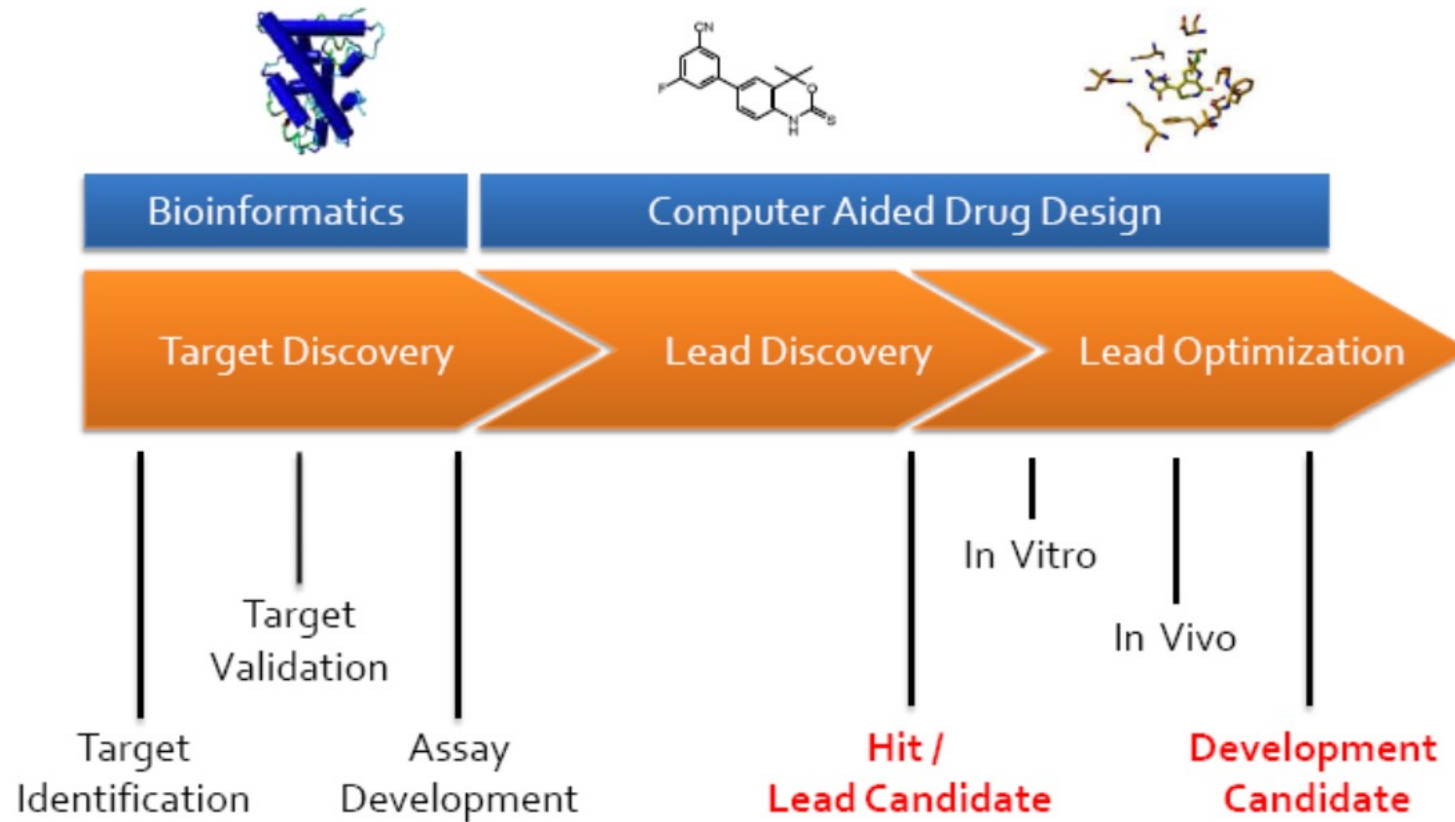


Dispondremos de vacunas de forma rápida - Serán seguras y eficaces



¿Seremos capaces de controlar el movimiento antivacunas?

Descubrimiento de nuevos fármacos



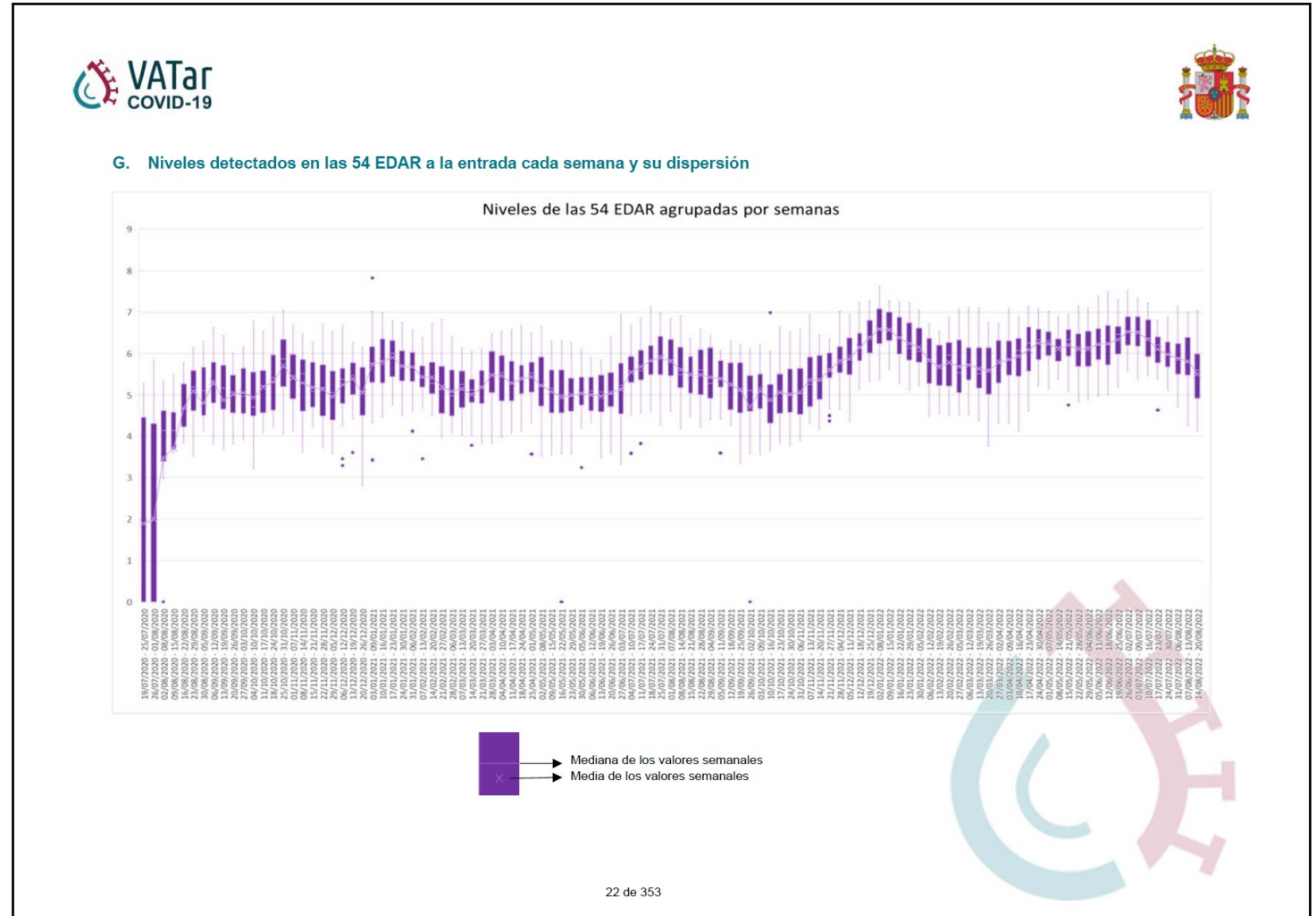
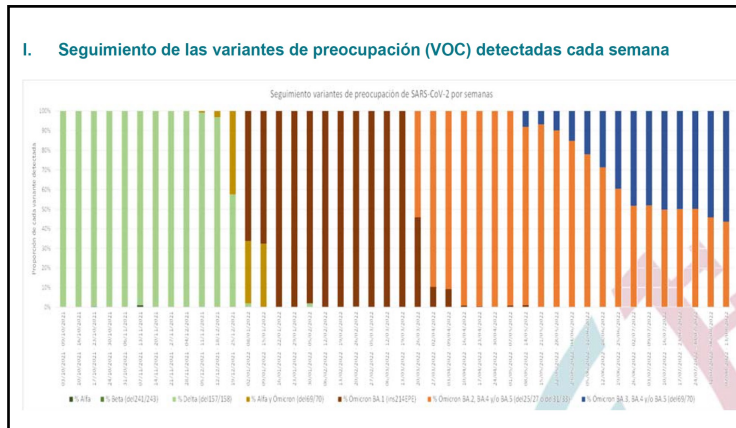
Dispondremos de fármacos seguros y eficaces gracias a la bioinformática y al diseño computacional

Desarrollo de métodos diagnósticos

GOBIERNO DE ESPAÑA
VICERREINADO CUARTA DEL GOBIERNO
MINISTERIO PARA LA TRANSICIÓN ECOLÓGICA Y EL RETO DEMOGRÁFICO
MINISTERIO DE SANIDAD

VATar COVID-19

CONTROL MICROBIOLÓGICO EN AGUAS RESIDUALES COMO INDICADOR EPIDEMIOLÓGICO DE ALERTA TEMPRANA DE PROPAGACIÓN DE COVID-19



POLIOMELITIS

Londres activa la vacunación urgente de un millón de niños contra la polio

Se trata de una dosis extra para los menores de uno a nueve años ante el inusual volumen del virus detectado en aguas residuales



Niños jugando junto al Támesis, en Londres, el 29 de julio.

HENRY NICHOLLS | REUTERS

Desarrollo de métodos diagnósticos

The screenshot shows the Weill Cornell Medicine Newsroom website. The top navigation bar includes a menu icon, the Weill Cornell Medicine logo, and links for Care, Discover, and Teach. The main header is "Newsroom" with sub-navigation for Home, News, Press Room, Publications, Video & Photography, Social Media, and About Us. The "News" sub-page is active, showing a breadcrumb trail "Home / News". The main article title is "USF Health, Weill Cornell Medicine Earn Inaugural Funding in NIH's Newly Launched Bridge2AI Initiative, will Create Artificial Intelligence Platform for Using Voice to Diagnose Disease". The article text states: "As one of four projects funded by NIH's Bridge2AI, this multi-institution project – co-led by the University of South Florida and Weill Cornell Medicine – will bring together medical, voice, AI, engineering, and ethics experts to create a human voice database using privacy-preserving AI, giving doctors a new tool for diagnosing conditions known to have associations with voice alterations." The date is "SEPTEMBER 13, 2022" and there is a "Back to News" button.

<https://news.weill.cornell.edu/news/2022/09/usf-health-weill-cornell-medicine-earn-inaugural-funding-in-nih's-newly-launched>

Mediante inteligencia artificial se diagnosticarán numerosas enfermedades

EPIDEMIOLOGY

The costs and benefits of primary prevention of zoonotic pandemics

Aaron S. Bernstein^{1*}, Amy W. Ando^{2,3}, Ted Loch-Temzelides⁴, Mariana M. Vale^{5,6}, Binbin V. Li^{7,8}, Hongying Li⁹, Jonah Busch¹⁰, Colin A. Chapman^{11,12,13,14}, Margaret Kinnaird¹⁵, Katarzyna Nowak^{16†}, Marcia C. Castro¹⁷, Carlos Zambrana-Torrel⁹, Jorge A. Ahumada¹⁰, Lingyun Xiao¹⁸, Patrick Roehrdanz¹⁰, Les Kaufman¹⁹, Lee Hannah¹⁰, Peter Daszak⁹, Stuart L. Pimm^{8*}, Andrew P. Dobson^{20,21*}

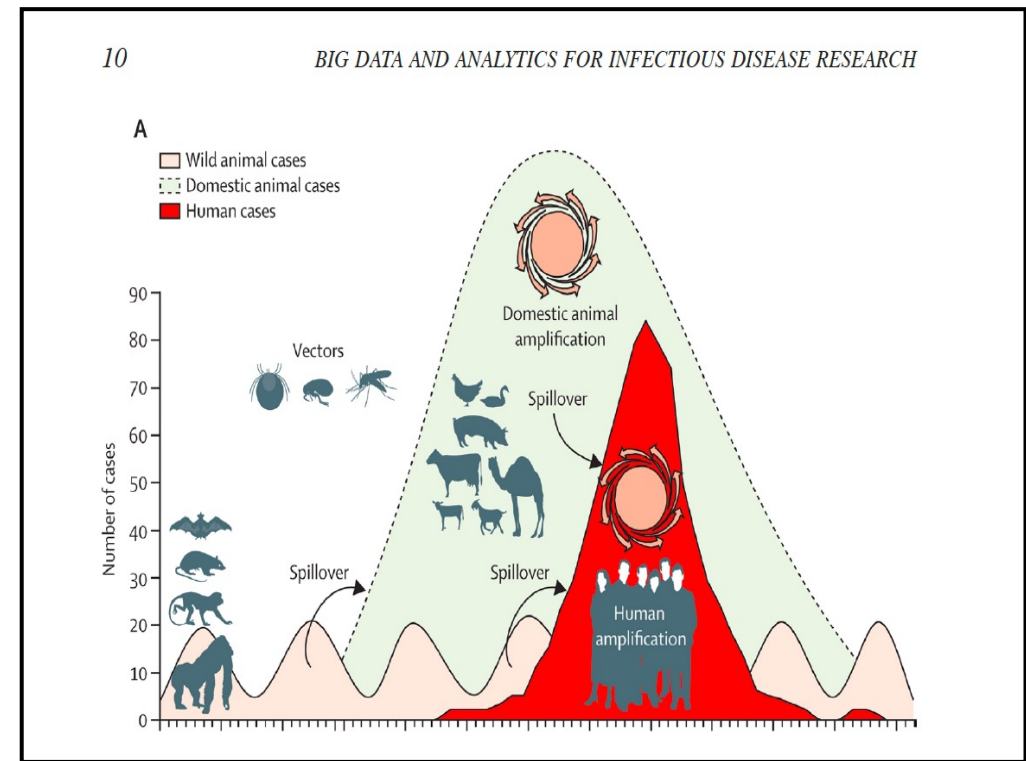
The lives lost and economic costs of viral zoonotic pandemics have steadily increased over the past century. Prominent policymakers have promoted plans that argue the best ways to address future pandemic catastrophes should entail, “detecting and containing emerging zoonotic threats.” In other words, we should take actions only after humans get sick. We sharply disagree. Humans have extensive contact with wildlife known to harbor vast numbers of viruses, many of which have not yet spilled into humans. We compute the annualized damages from emerging viral zoonoses. We explore three practical actions to minimize the impact of future pandemics: better surveillance of pathogen spillover and development of global databases of virus genomics and serology, better management of wildlife trade, and substantial reduction of deforestation. We find that these primary pandemic prevention actions cost less than 1/20th the value of lives lost each year to emerging viral zoonoses and have substantial cobenefits.

Sci. Adv. **8**, eabl4183 (2022) 4 February 2022

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original U.S. Government
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“Utilización del Big Data” - The PREDICT Strategy

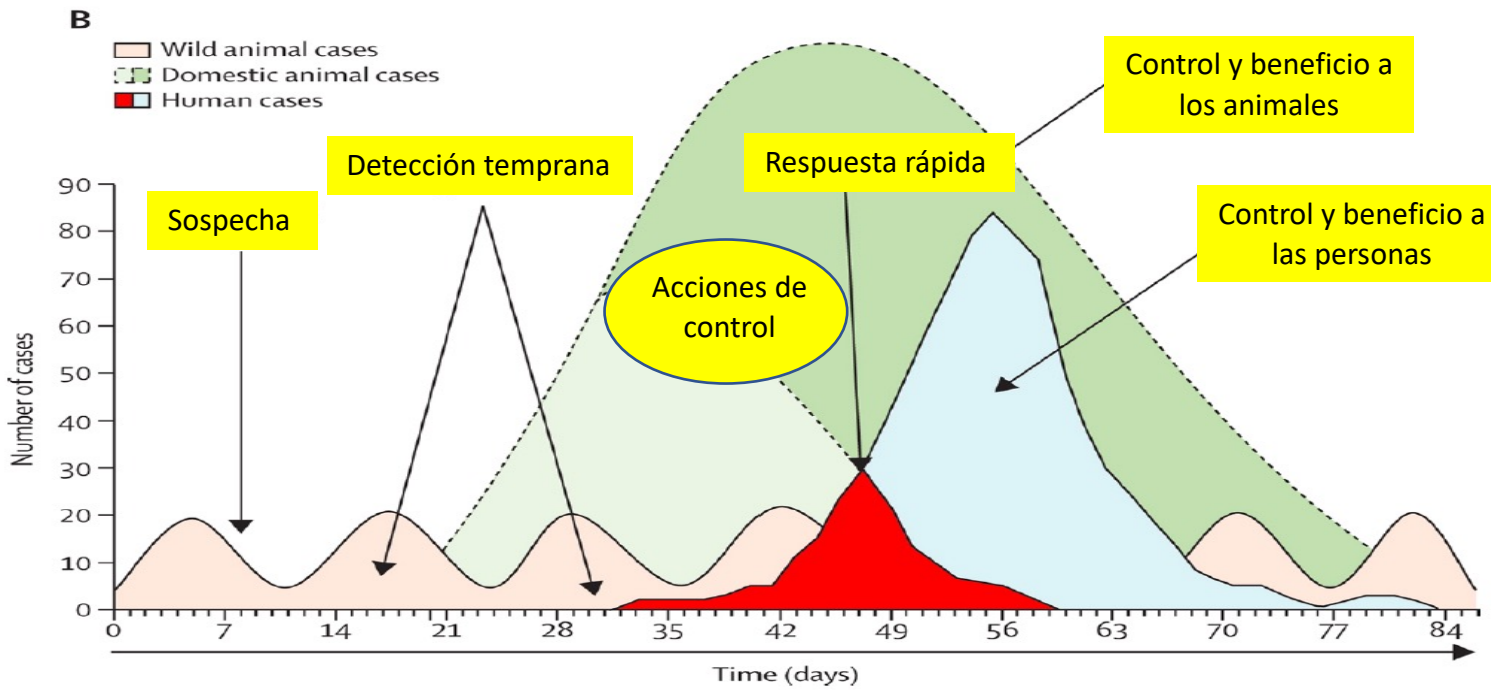
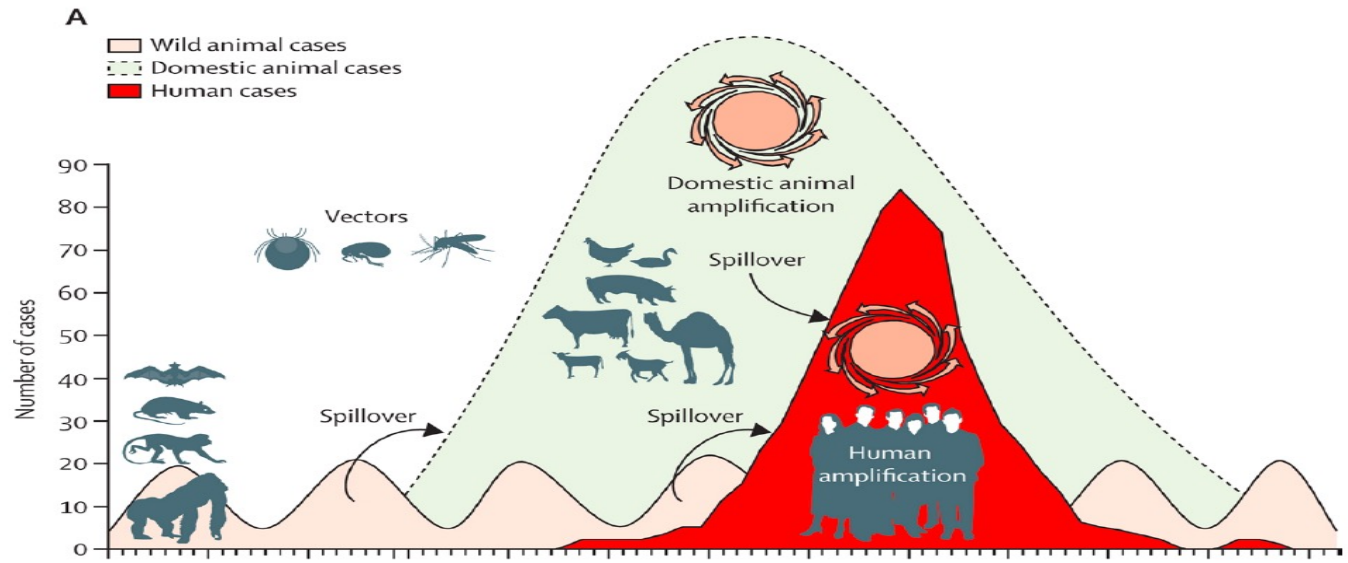
- El 75% de todas las infecciones emergentes y re-emergentes que están afectando a humanos en el siglo XXI son zoonóticas.
- Entre 1990 y 2010, el 91% de las infecciones emergentes se propagaron a partir de un foco animal silvestre.



Big data and analytics for infectious diseases research, operations and policy 2016

Ecology of zoonoses: natural and unnatural histories Karesh et al. Lancet 2012

Generar información sobre la presencia de microorganismos en animales silvestres y artrópodos puede permitir el diseño de estrategias antes de que se transmitan al hombre



Proyecto Viroma Global



REASONING

GVP is a ten-year project to pre-empt emerging pandemic threats by identifying the majority of unknown viruses throughout the world that are likely to infect humans.



BENEFITS

GVP will revolutionize the way we think about emerging infectious disease, including biomedical countermeasures and food security.



DELIVERABLES

GVP will deliver multiple, quantifiable and observable benefits to the world as well as move epidemiological science into the future.

<https://www.globalviromeproject.org/why-we-exist>

El proyecto viroma global es una iniciativa científica cooperativa para reducir de forma masiva el riesgo de futuras epidemias y brotes epidémicos

Bioterrorismo

Israel se prepara para un ataque terrorista biológico

23.11.2011 08:49 |



[Ver más imágenes»](#)

Los ministerios de defensa y salud llevarán a cabo un ejercicio llamado "Llama Naranja 6" en el norte la semana que viene y simularán un ataque terrorista "no convencional".

La actividad de dos días el miércoles y el jueves recrearán un brote de una enfermedad contagiosa que atacaría e infectaría las ciudades del norte, principalmente Afula, Tiberias y el área de Nazareth en Galilea.

El Ministerio de Defensa tiene intenciones de llevar a cabo simulacros adicionales en el campo del terrorismo no convencional en el próximo año.

El ejercicio testeará y entrenará a los operativos del Ministerio de Defensa, Relaciones Exteriores, Medio Ambiente y Salud, y al Comando de Seguridad Interna, gobiernos locales, policía, servicios de rescate, hospitales, y Autoridades Acuíferas.

Las autoridades locales armarán Centros de Tratamiento de

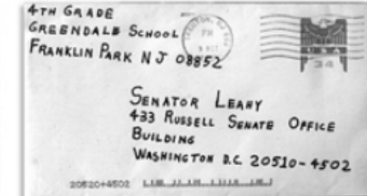
Profilaxis Masivo, que simularán la provisión de un tratamiento preventivo a los ciudadanos que se sospecha que fueron expuestos al brote. Cada centro será ejercitado dentro de sus capacidades de tratar aproximadamente a 5.000 por día. "Es importante que los ciudadanos de Israel sepan que hay personas en el establecimiento de defensa, así también como otras autoridades relevantes, que tienen el trabajo permanente de preparar al Estado de Israel para manejar este tipo de situaciones", dijo el brigadier general Ze'ev Snir, quien es ministro asistente de defensa química, biológica, radiológica y nuclear.



SPECIAL REWARD
Up to **\$2.5 million**



For information leading to the arrest and conviction of the individual(s) responsible for the mailing of letters containing anthrax to the New York Post, Tom Brokaw at NBC, Senator Tom Daschle and Senator Patrick Leahy:



**AS A RESULT OF EXPOSURE TO ANTHRAX,
FIVE (5) PEOPLE HAVE DIED.**

The person responsible for these deaths...

- Likely has a scientific background/work history which may include a specific familiarity with anthrax
- Has a level of comfort in and around the Trenton, NJ area due to present or prior association

Anyone having information, contact **America's Most Wanted at 1-800-CRIME TV** or the **FBI** via e-mail at amerithrax@fbi.gov

All information will be held in strict confidence. Reward payment will be made in accordance with the conditions of Postal Service Reward Poster 296, dated February 2000. Source of reward funds: U.S. Postal Service and FBI \$2,000,000; ADVO, Inc. \$500,000.

Autoridad de Preparación y Respuesta ante Emergencias Sanitarias



Comisión Europea - Comunicado de prensa



**Unión Europea de la Salud: la HERA presenta la lista de las tres mayores
amenazas para la salud contra las que debemos prepararnos**

Bruselas, 12 de julio de 2022

https://ec.europa.eu/commission/presscorner/detail/es/ip_21_4672

Amenazas contra las que tenemos que prepararnos

Categorías de amenazas transfronterizas graves para la salud detectadas

1. **Patógenos con alto potencial pandémico:** incluye el examen de familias víricas específicas preocupantes, teniendo en cuenta también la naturaleza zoonótica de la mayoría de las enfermedades infecciosas emergentes de consecuencias graves. Esta categoría comprende principalmente familias de virus de ARN que afectan al aparato respiratorio.
2. **Amenazas químicas, biológicas, radiológicas y nucleares:** su origen puede ser una liberación accidental o deliberada, teniendo en cuenta las tensiones geopolíticas mundiales, así como incidentes causados por agentes que actúen de manera negligente. Las sustancias de esta categoría se han determinado en función de sus probabilidades de liberación y de los posibles efectos para la salud humana.
3. Las amenazas derivadas de la **resistencia a los antibióticos**, que suponen uno de los mayores riesgos para la salud humana, ya que la resistencia antibacteriana por sí sola provoca, según las estimaciones, más de 1,2 millones de muertes anuales en todo el mundo.




¿Serán sensibles los políticos?

¿Seguirán las recomendaciones técnicas?

Commission Statement

Lancet 2020; 396: 1102-24

Published Online
September 14, 2020
[https://doi.org/10.1016/S0140-6736\(20\)31927-9](https://doi.org/10.1016/S0140-6736(20)31927-9)

 **Lancet COVID-19 Commission Statement on the occasion of the 75th session of the UN General Assembly**

The Lancet COVID-19 Commissioners, Task Force Chairs, and Commission Secretariat

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7489891/pdf/main.pdf>

Amenaza de emergencia de nuevos SARS-CoV

SARS-CoV

¿Otro CoV?

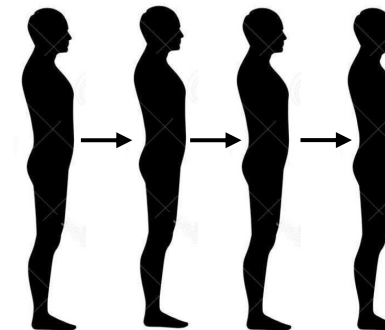


Co-Infección en otro animal

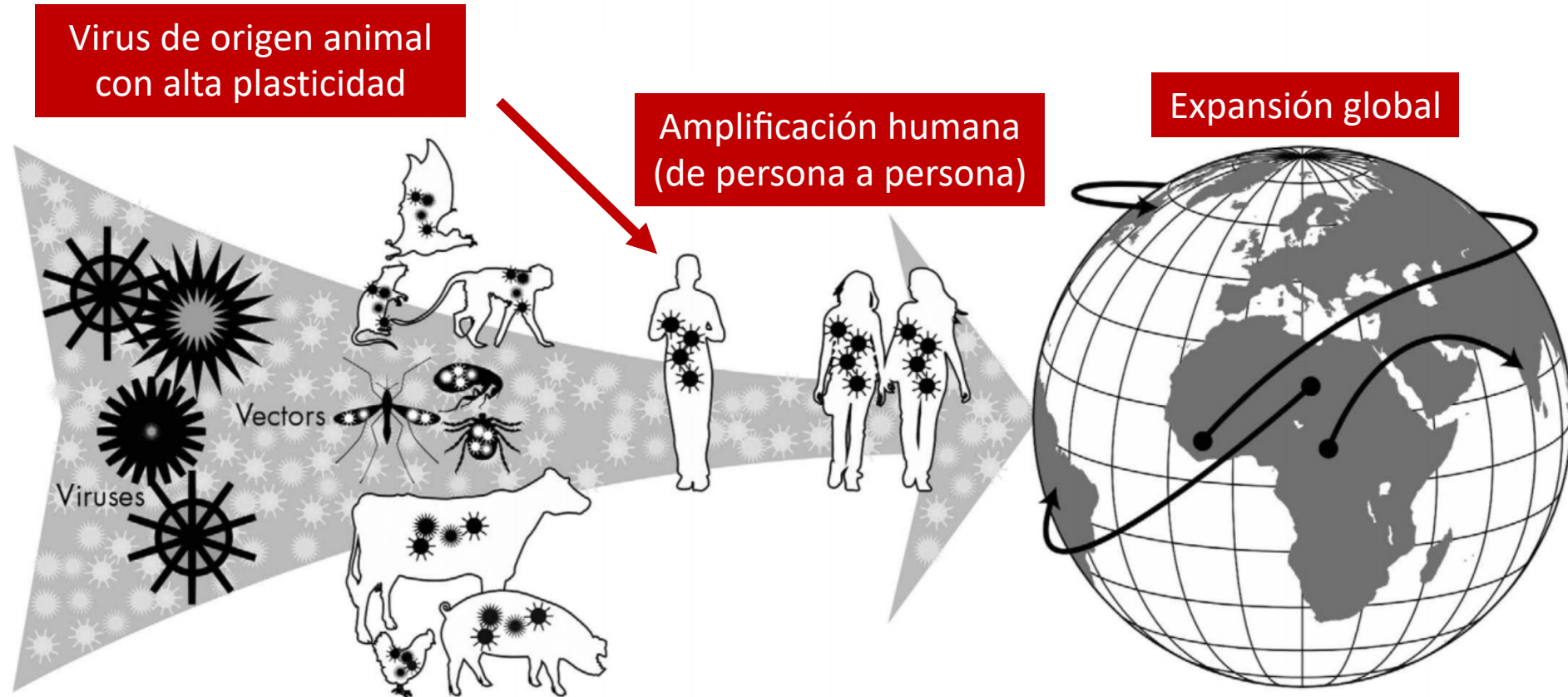
Amplificadores
Hospedadores intermedios

Nuevo (recombinante)
SARS-CoV

'Spillover'



¿Cuál será el agente de la nueva enfermedad X?



¿Hacemos apuestas?

Amenaza de brotes de Gripe de Aviar con capacidad Pandémica

News > Reuters Health Information

Proliferation of Bird Flu Outbreaks Raises Risk of Human Pandemic

By Kate Kelland

January 27, 2017



La OMS y la FAO advierten que el brote de gripe aviar alcanza dimensiones nunca vistas

«Hay que prepararse para una eventual pandemia», sostiene la OMS

Vietnam registró dos nuevas víctimas, alcanzando un total de 17 en Asia

AGENCIAS. ROMA

«La epidemia no está todavía bajo control, la situación es seria y hace falta una respuesta de emergencia». Este fue el agrio diagnóstico sobre la 'gripe del pollo' dictado ayer por la FAO, la Organización de las Naciones Unidas para la Agricultura y la Alimentación.

La cumbre de expertos celebrada esta semana en Roma para coordinar esa reacción urgente ha concluido que, de momento, la única solución es seguir con el sacrificio de animales enfermos, que hasta ahora ha eliminado 50 millones de ejemplares. Luego, cuando por fin haya vacunas, se podrá combinar con una campaña de pro-

tección. Según la FAO eso será dentro de «algunos meses», al menos tres. Una partida de 1.000 dosis costará en torno a los 50 dólares.

Dos muertos más

Hasta entonces no se sabe qué va a pasar. El número de muertos se elevó ayer a 17, con dos nuevas víctimas en Vietnam. Junto a Tailandia, son los dos únicos países donde el hombre se ha contagiado del virus, mientras otros ocho, siempre en Asia, lo han detectado en sus granjas.

A la vista de la situación, la Organización Mundial de la Salud (OMS), también presente en la reunión de Roma, confirma que la enfermedad se extiende cada vez más y que se está preparando «para

afrontar una eventual pandemia»: una oleada de contagios de personas que han estado en contacto con animales o, la peor hipótesis posible, la transmisión del virus entre humanos.

Sin embargo, esta amenaza aún no se ha hecho realidad. La cumbre de Roma ha constatado que el virus de la gripe aviar no ha mutado, todos sus genes son de origen animal y, por tanto, no se adapta al hombre. Salvo en casos excepcionales, no logra 'saltar' de una persona a otra. «La evolución del virus se actualiza de hora en hora», asegura la OMS.

La lucha contra la 'gripe del pollo' requerirá también mucho dinero, advierten los organismos internacionales, y sobre todo, la colaboración de los países afectados. «Hay que indemnizar a los campesinos, financiar los equipos de protección, incidir en la formación y reforzar los controles en las granjas y de los movimientos de animales», precisaron, indicando que estas tareas corresponden a los países afectados.

Alertas continuas en todo el mundo de brotes de gripe aviar con casos aislados/brotes humanos

Numero acumulado de casos de Gripe Aviar (A/H5N1 2003-2021)

Country	2003-2009*		2010-2014*		2015-2019*		2020		2021		Total	
	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths
Azerbaijan	8	5	0	0	0	0	0	0	0	0	8	5
Bangladesh	1	0	6	1	1	0	0	0	0	0	8	1
Cambodia	9	7	47	30	0	0	0	0	0	0	56	37
Canada	0	0	1	1	0	0	0	0	0	0	1	1
China	38	25	9	5	6	1	0	0	0	0	53	31
Djibouti	1	0	0	0	0	0	0	0	0	0	1	0
Egypt	90	27	120	50	149	43	0	0	0	0	359	120
Indonesia	162	134	35	31	3	3	0	0	0	0	200	168
Iraq	3	2	0	0	0	0	0	0	0	0	3	2
Lao People's Democratic Republic	2	2	0	0	0	0	1	0	0	0	3	2
Myanmar	1	0	0	0	0	0	0	0	0	0	1	0
Nepal	0	0	0	0	1	1	0	0	0	0	1	1
Nigeria	1	1	0	0	0	0	0	0	0	0	1	1
Pakistan	3	1	0	0	0	0	0	0	0	0	3	1
Thailand	25	17	0	0	0	0	0	0	0	0	25	17
Turkey	12	4	0	0	0	0	0	0	0	0	12	4
Viet Nam	112	57	15	7	0	0	0	0	0	0	127	64
Total	468	282	233	125	160	48	1	0	0	0	862	455

* 2003-2009, 2010-2014 and 2015-2019 total figures. Breakdowns by year available on subsequent tables.

Total number of cases includes number of deaths.

WHO reports only laboratory-confirmed cases.

All dates refer to onset of illness.

Source: WHO/GIP, data in HQ as of 15 April 2021



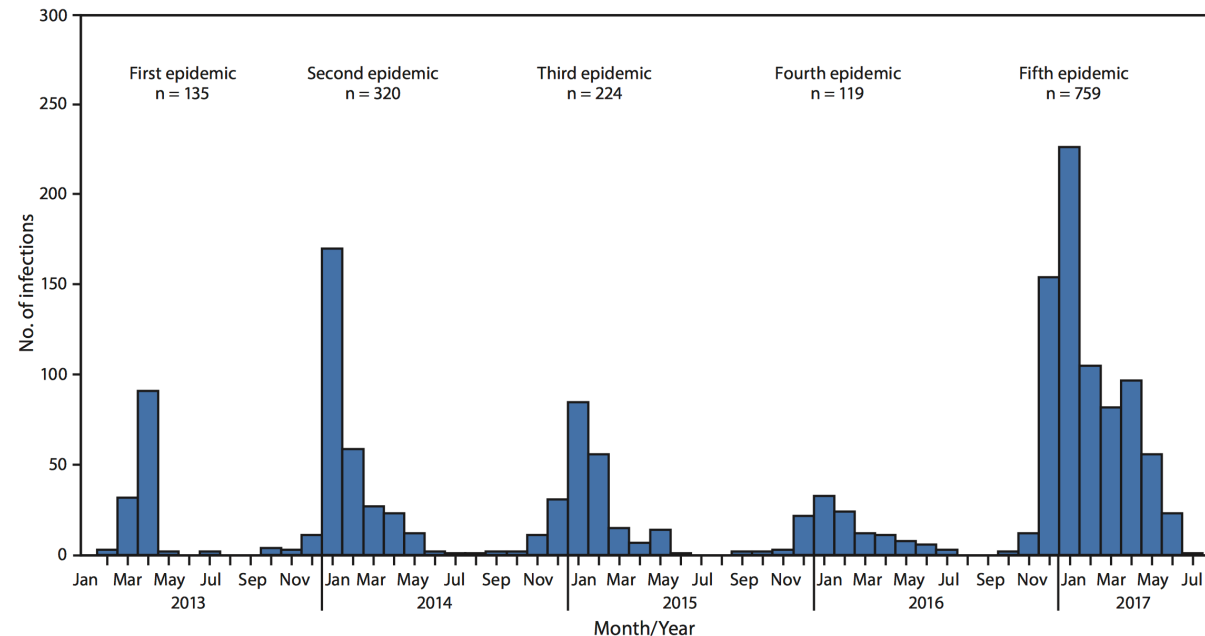
https://cdn.who.int/media/docs/default-source/influenza/h5n1-human-case-cumulative-table/2021_april_tableh5n1.pdf?sfvrsn=fc40672c_5&download=true

Numerosos episodios de *Spillover* a humanos aunque la transmisión inter-humanos ha sido puntual

Update: Increase in Human Infections with Novel Asian Lineage Avian Influenza A(H7N9) Viruses During the Fifth Epidemic — China, October 1, 2016–August 7, 2017

James C. Kile, DVM^{1,2}; Ruiqi Ren, MPH^{2,3}; Liqi Liu, MPH⁴; Carolyn M. Greene, MD⁵; Katherine Roguski, MPH¹; A. Danielle Iuliano, PhD¹; Yunho Jang, PhD¹; Joyce Jones, MS¹; Sharmi Thor, PhD¹; Ying Song, MD⁵; Suizan Zhou, MPH⁵; Susan C. Trock, DVM¹; Vivien Dugan, PhD¹; David E. Wentworth, PhD¹; Min Z. Levine, PhD¹; Timothy M. Uyeki, MD¹; Jacqueline M. Katz, PhD¹; Daniel B Jernigan, MD¹; Sonja J. Olsen, PhD¹; Alicia M. Fry, MD¹; Eduardo Azziz-Baumgartner, MD¹; C. Todd Davis, PhD¹

FIGURE 1. Confirmed Asian lineage avian influenza A(H7N9) virus infections of humans reported to the World Health Organization (N = 1,557)* by month of illness onset — China,† February 19, 2013–August 7, 2017

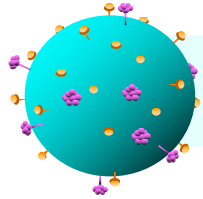


¿Cuál será?

H5N1; H7N9; otro?

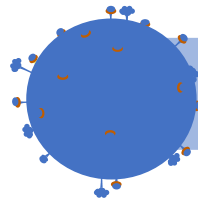
Pandemias Gripales durante el siglo XX y XXI

Gripe Española



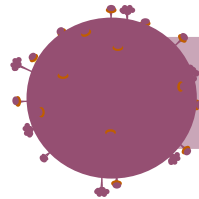
H1N1

Gripe de Hong Kong



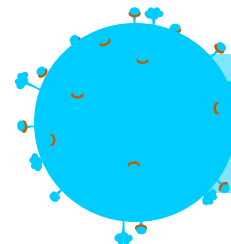
H3N2

Gripe Asiática

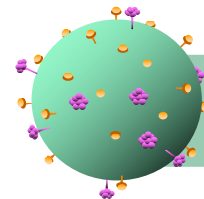


H2N2

Gripe Porcina



H1N1



??

1918

1957

1968

2009

2022

☰ EL PAÍS

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GRUPE AVIAR >

Un enorme brote de gripe aviar para cerrar la campaña de las macrogranjas

El virus, que está golpeando a España desde hace unas semanas, obliga a sacrificar más de 130.000 gallinas en una macroexplotación de Valladolid. Greenpeace pide que el nuevo Gobierno de Castilla y León decrete una moratoria a la ganadería industrial

☰ LAVANGUARDIA 🔔

Natural

INFECCIÓN PREOCUPANTE

Macrogranja devastada por la gripe aviaria: imágenes de un peligro que se extiende

- Cuatro nuevos focos en granjas en una semana, que se suman a 2 anteriores y a los 12 focos en aves silvestres
- La gripe aviaria sigue salpicando en España: segundo foco en una granja, en Huelva

Detectan hasta seis brotes de gripe aviar en diferentes granjas españolas este año

El sacrificio de 133.750 gallinas ponedoras en una explotación de Valladolid pone el foco sobre el origen de estas infecciones



Sacrificio de 133.750 gallinas ponedoras en una granja de Íscar, en Valladolid. / EFE

Solo en España detectados en 2022 —————> 85 focos en aves silvestres y 36 en explotaciones avícolas



SECRETARIA GENERAL DE
SANIDAD Y CONSUMO

DIRECCIÓN GENERAL DE
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INNOVACIÓN

**Centro de Coordinación de Alertas y
Emergencias Sanitarias**

EVALUACIÓN RÁPIDA DE RIESGO

Primera detección de gripe aviar A(H5N1) en humanos en España

4 de octubre de 2022

THE
BEATLES

Tomorrow never knows



THE
BEATLES



«Tomorrow Never Knows»

Canción de The Beatles

Álbum	<i>Revolver</i>
Publicación	5 de agosto de 1966
Grabación	EMI Studios, Londres (6, 7 y 22 de abril de 1966)
Género	Rock psicodélico, ^{1 2} rock experimental, ³ Art rock Raga rock Drone rock Avant-pop
Duración	2:57
Discográfica	Parlophone
Escritor(es)	Lennon-McCartney
Productor(es)	George Martin
Idioma original	inglés

Mañana nunca se sabe